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(71) Applicant: **SCLAVO S.p.A.**  
**Via Fiorentina 1**  
**I-53100 Siena(IT)**

(72) Inventor: **Ratti, Giulio**  
**Strada di Vico Alto, 6**  
**I-53100 Siena(IT)**  
Inventor: **Comanducci, Maurizio**  
**Via Montanini, 54**  
**I-53100 Siena(IT)**  
Inventor: **Tecce, Mario F.**  
**Via Mino Celsi, 12**  
**I-53010 Costalfino (Siena)(IT)**  
Inventor: **Giuliani, Marzia M.**  
**Via Garibaldi, 58**  
**I-53034 Colle val d'Elsa (Siena)(IT)**

(74) Representative: **Moretti, Giorgio et al**  
**Notarbartolo & Gervasi s.r.l. Viale Bianca**  
**Maria, 33**  
**I-20122 Milano(IT)**

(54) **PCTD plasmid isolated from chlamydia trachomatis serotype D, its genes and proteins encoded by them; recombinant plasmids for the expression of said genes in heterologous systems as fused recombinant proteins, preparation of said recombinant proteins and their use in the formulation of vaccines and/or diagnostics.**

(57) **A plasmid isolated from *Chlamydia trachomatis* is described, which comprises 8 genes encoding proteins useful in the formulation of vaccines or diagnostic test for determining the bacterium or specific antibodies generated during *C. trachomatis* infections; in particular the recombinant fusion MS2-pgp3D protein is described comprising polypeptidic sequences encoded by pCT and immunogenic in the course of infections in man. A method for preparing said protein in *E.coli* further described.**

EP 0 499 681 A1

Invention Field

This invention refers to the pCTD plasmid isolated from *Chlamydia trachomatis* serotype D, cloned and sequenced and to the genes present in said plasmid, to the proteins expressed by said genes, to the expression vectors containing said genes and to the microorganisms transformed by said vectors. The invention further refers to the process for the preparation of genes and of said vectors and to the use of said proteins as antigens for the preparation of polyclonal and monoclonal antibodies apt to recognize *Chlamydia trachomatis* and hence useful for the preparation of vaccines capable of imparting a protective immunity against infections caused by *Chlamydia trachomatis* and pathologic conditions deriving from said infections and for the development of diagnostic methods for the search of specific antibodies produced following *C. trachomatis* infections.

Prior art

*Chlamydias* are gram-negative bacteria, obligate intracellular parasites of eukariotic cells. *Chlamydias* show an extracellular infective and metabolically practically inert form, called elemental body (EB), and intracellular replicative forms called reticular bodies (RB).

The reticular bodies, after multiplication by binary fission, are transformed into elemental bodies which come out of the host cell and infect new cells.

The masses or mini-colonies of reticular and elemental bodies inside an infected cell constitute the characteristic "inclusions" visible at the optical microscope.

*Chlamydia trachomatis* (*C. trachomatis* or CT), a bacterial species pathogenic to man, is the etiological agent of venereal lymphogranuloma (VLG), of various inflammatory pathologies of the genital male and female apparatus and of trachoma, a chronic disease which affects 500 million people and can lead to blindness.

In the technical literature ca. 15 CT serotypes pathogenic to man were described and divided in two groups which differ both as to virulence and tissular tropism.

Twelve serotypes of the trachoma group (biovar) are identified as A to K and infect, in general, epithelial tissues, such as the ocular (trachoma) and uro-genital (cervicitis and urethritis) mucous membranes, and show a low virulence.

The venereal lymphogranuloma (VLG) serotypes (L<sub>1</sub>, L<sub>2</sub> and L<sub>3</sub>) cause instead an infection of the reticulo-endothelial tissue, mainly of the inguinal and femoral lymphonodi, and are highly invasive.

Urethritis and cervicitis induced by CT (A to K serotypes) when not precociously diagnosed and treated by adequate therapy, may led to a variety of chronic inflammations, such as, e.g., vaginitis, salpingitis and pelvic inflammation which may resolve in sterility and extrauterine pregnancy.

Furthermore the new born from infected mothers may contract pulmonary and/or ocular infections during delivery.

For said reason it is necessary to possess adequate diagnostic methods for determining CT and formulating effective vaccines against said bacterium.

As known, factors which determine the bacterial virulence are often encoded by genes present on plasmids.

In the literature, the presence is reported, in all 15 serotypes and in the clinical isolates examined up to now, of a plasmid of ca. 7.5 Kb referred to in the present invention as pCT followed by the denomination of the bacterial serotype concerned. For example: pCTD for the plasmid isolated from serotype D, etc.

Up to now, however, no specific function or products encoded by it were associated with said plasmid.

Detailed description of the invention

A variant of the plasmid, corresponding to serotype D, was now isolated, indicated in what follows a pCTD, which comprises at least eight genes encoding for new proteins.

Figure 1a shows the nucleotidic sequence of said plasmid and 7 of the 8 protein structures expressed by said sequence. The eighth protein structure, encoded on the DNA chain complementary to the one of Fig. 1a, is shown in Fig. 1b.

Object of the present invention are thus: the cloned and sequenced pCTD plasmid, the nucleotide sequences encoding for the above named proteins, the expression vectors containing one of said sequences or fragments thereof.

Further object of the present invention are the pCTD proteins or fragments of them having immunogenic properties.

Still another object of the present invention are the fusion polypeptides comprising one of said proteins or its fragments suitable as antigens.

The present invention further refers to the preparation of said proteins and of their fragments possessing immunogenic activity or of fused polypeptides comprising said proteins.

5 Said proteins, their fragments or fusion polypeptides comprising said proteins or their fragments, according to the invention may be employed to determine the CT produced infections in biological samples.

Said proteins, their fragments or fusion polypeptides comprising the protein or its fragments may further be employed, according to the invention, as antigens useful in the formulation of vaccines against infections due to CT.

10 According to the invention, said proteins, their fragments or fusion polypeptides may be used furthermore as antigens for the preparation of poly- or mono-clonal antibodies to be used in diagnostics. In particular, the present invention relates to the pgp 3D protein encoded by the gene of the pCTD plasmid identified as ORF3D having the nucleotide sequence reported in Fig. 2, and characterized by a molecular weight of 27,802 and by the aminoacid sequence reported in Fig. 2.

15 According to the present invention, plasmid pCTD is obtained from the *C.trachomatis* GO/86 strain isolated from the urethra of a patient with non-gonococcal urethritis, and successively identified as serotype D by the immunofluorescence method described by Wang, S.P. and Grayston, J.T. [Am. J. Ophthalmol. 70: 367-374 (1970)]. The ORF3D gene may be isolated from the pCTD plasmid employing one of the known methods such as, e.g., the in vitro amplification method [Saiki, A.K. et al. Science, 239 :487-491 (1988)]  
20 using as primers synthetic oligonucleotides having a primary structure suitably derived from the sequence data shown in Figs. 1a and 1b. The thus amplified gene is then cloned in a vector placing it under the control of sequences regulating its expression.

One can similarly proceed for the other seven genes the nucleotide sequences of which are reported in Figs. 1a and 1b.

25 The proteins encoded by said genes are represented by the aminoacid sequences also reported in Figs. 1a and 1b.

Vectors suitable for the ends of the present invention may be plasmids with expression in host cells selected among the ones known and available commercially or at authorized collection centers.

30 The cells transformed by said vectors are then cultivated in a suitable culture medium in the presence of carbon-, nitrogen- and mineral salts sources, possibly in induction conditions, at a temperature and time period selected in order to obtain the production of the desired protein.

Said protein, obtainable also as fused polypeptide, constituted by a polypeptide produced by the vector fused with the protein itself, is then separated and purified from the culture medium or from the cell lysate.

35 According to one embodiment of the present invention, the ORF3D gene is cloned in the plasmidic *E.coli* pEX34a vector, a derivative of pEX29 and pEX31 described by Strebel et al. [J.Virol., 57:983-991 (1986)], following the description by Nicosia et al. in Infect. Imm. 1987, Vol.55, 963-967.

40 The results show the presence in the bacterial extracts of a polypeptide, indicated as MS2-pgp3D, the sequence of which is shown in Fig. 3, with a mol. weight of ca. 39 Kd, consisting i.e. of a RNA-polymerase fragment of bacteriophage MS2, produced by the expression system of ca. 11 Kd and by the protein encoded by the ORF3D gene of ca. 28 Kd.

Said polypeptide employed as antigen in a Western-Blot assay, or in immunologic assays, is recognized by antibodies present in the serum of patients with CT infection and may further be employed for the production, in laboratory animals, of mono- and poly-clonal antibodies which recognize the - and react with the corresponding pgp3 protein, in all its variants, of *C.trachomatis*.

45 In accordance with the present invention the pCTD and p03/60/MCI plasmids were deposited as ATCC N° 68314 and ATCC N° 68315 respectively.

The experimental examples that follow are illustrative and non limitative of the invention.

## EXAMPLE 1

50

### Isolation of the pCTD plasmid from *C.trachomatis* GO/86

55 *C.trachomatis* cells were isolated following known techniques from the urethra of a patient with non-gonococcal urethritis. The strain, identified as serotype D by the micro-immunofluorescence technique described by Wang, S.P. and Grayston, J.T. [(1970), Am. J. Ophthalmol., 70: 367-374] is designated as GO/86.

The elemental bodies of said strain are then purified as described by Cevenini R. et al. [(1988), FEMS Microbiol. Letters, 56:41-46] on renografin<sup>R</sup> density discontinuous gradients (E.R. Squibb & Sons, Princeton,

N.J.) according to what reported by Caldwell H.D. et al. [(1988) Infect. Immun. 31:1161-1176].

After purification, the elemental bodies (ca. 1.5 mg proteins) are lysated by incubation in 10 mM Tris-HCl, pH 8.0, 150 mM NaCl, 2mM EDTA, 0.6% SDS and 100 mg/ml K Proteinase (Boehringer) at 37° C for 3 hrs. The total nucleic acids are then extracted with phenol/chloroform, precipitated with ethanol, treated with

pancreatic RNase (250 ng/μl final concentration), further precipitated with ethanol and re-suspended in 800 μl water (365 ng/μl of DNA).  
A 10 μl aliquot of said solution is then treated with 30 units (U) of BamHI restriction enzyme (Boehringer) at 37° C for 2 hrs in 20 μl (final volume) of a digestion mixture suggested by the supplier. 3 μl of the resulting digestion mixture are ligated to 100 ng plasmidic pUC8 DNA previously digested with BamHI and dephosphorilated with calf gut phosphatase. The ligase reaction is effected overnight in 20 μl buffer containing 9 U T4 DNA ligase (Boehringer) at 18° C.

The ligation mixture is then employed to transform HB101 E.coli cells made competent by a treatment with CaCl<sub>2</sub> as described by Mandel and Higa [(1970) J. Mol. Biol. 53, 54]. The transformants are selected on LB agar Medium (DIFCO) with addition of 100 μg/ml ampicillin, at 37° C overnight.

The positive clones (ampicillin resistant) (Amp<sup>R</sup>) containing, that is, the recombinant pUC8 plasmid are transferred onto Hybond-N membranes (Amersham) and sorted by hybridization with three <sup>32</sup>P marked oligonucleotides having the following nucleotidic sequences:

- 1) 5'ATGGGTAAAGGGATTTTATC3'
- 2) 5'CTATATTAGAGCCATCTTC3'
- 3) 5'TCAAAGCGCTTGCACGAAG3'

The above reported oligonucleotides are synthesized by means of an automatic synthesizer (Applied Biosystem Inc. Mod. 380A) following the methods and employing the reagents recommended by the manufacturers.

Four of the six plasmids isolated from the clones found positive at the hybridization, analyzed by electrophoresis on agarose 1% gel before and after digestion with BamHI are found to consist of the pUC8 plasmid nucleotidic sequence and of a nucleotidic insert of ca. 7.5 kilobases corresponding to the isolated C.trachomatis GO/86 plasmid.

The nucleotidic sequences of said insert is determined according to the method of Sanger F. [(1977) PNAS USA 74:5463-5467] utilizing a series of suitable primers. The sequencing reactions are performed on double helix DNA employing the Sequenase Kit (U.S. Biochemical Co. Cleveland, Ohio) as recommended by the firm.

The nucleotidic sequences of the ca. 7.5 kilobases plasmid named pCTD are reported in Figs. 1a and 1b. The recombinant plasmid containing said insert is indicated as pUC8-pCTD.

## EXAMPLE 2

### Cloning of the DNA ORF3D segment of plasmid pCTD1D

The DNA fragment denoted as ORF3D(Fig. 2) of 792 bp is obtained through in vitro amplification according to the technique known as Polymerase Chain Reaction (PCR) described by Saiki A.K. et al. [(1988) Science 239:487-491].

The amplification is effected utilizing ca. 10 ng of the pUC8-pCTD plasmid and employing as primers two synthetic oligonucleotides (ORF31) and (ORF3dx) having respectively the following nucleotide sequences:

- 5' CAGGGATCCATGGGAAATTCTGGTTTTT3'

BamHI

5

- 5' CCCCTGCAGTTAAGCGTTTGTGTTGAGGT3'

Pst I

10 Said oligonucleotides are complementary to ORF3 regions with the addition to the respective 5' terminals of a nucleotide sequence comprising the action site of a restriction enzyme selected among the ones present in the pEX34A vector (Strebel K. et al. [(1986) J. Virol. 57: 983-991] utilized for the successive cloning. In particular, the site selected for ORF31 is the one for the BamHI enzyme, while for ORF3dx is the one of the PstI enzyme.

15 The amplification reaction is performed employing the reagents contained in the "Geneamp" Kit (Perkin Elmer-Cetus). 25 amplification cycles are effected. Each amplification cycle consists in heating the reaction mixture to 94 °C for one minute, to 50 °C for one minute and finally to 72 °C for one minute.

At the end of the amplification reaction the mixture is extracted, in succession, with an equal volume of phenol and of a chloroform-isoamyl alcohol mixture (24:1 v/v) and then submitted to forced dialysis by means of Centricon<sup>R</sup> cartridges following the producer's (Amicon) instructions.

20 The DNA is then precipitated by adding to the obtained solution sodium acetate 3 M, pH 5.5 (1/10 of the volume) and cold (-20 °C) ethanol (3 vols.). The DNA precipitate is dissolved in 44 µl water. To the solution, 5 µl H buffer (Boehringer) and 1 µl PSTI restriction enzyme (20 units/µl) are added and the DNA is digested at 37 °C for 2 hours.

25 The digestion mixture is then extracted with phenol, chloroform/isoamyl alcohol and then the DNA is precipitated with ethanol (-20 °C). The precipitate, separated by centrifugation, is suspended again in 44 µl water and then digested with 20 U BamHI in 5 µl of B buffer (Boehringer) at 37 °C for 2 hours. The digestion mixture is extracted with phenol, chloroform/isoamyl alcohol and dialyzed by Centricon<sup>R</sup> cartridge.

30 At the same time, 10 µg of the pEX34A plasmidic vector are digested with the PstI and BamHI restriction enzymes as reported supra. The vector is dephosphorylated with alkaline phosphatase, extracted with phenol and chloroform/isoamyl alcohol, precipitated with ethanol (-20 °C) and re-suspended in 50 µl water.

35 1 µl (100 ng) of the vector and 2 µl (200 ng) of the amplified ORF3D segment are then ligated in 2 µl ligase buffer to which 2 µl ATP r, 1 µl T4 DNA ligase (9 units/µl) are added, adding water to a total volume of 20 µl. The ligase reaction is performed at 15 °C overnight. The ligase mixture is employed to transform 200 µl of a suspension of *E. coli* competent cells (K12-ΔH1-Δ trp) [Remaut E. et al. (1983), Gene 22:103-113]. After treatment at 30 °C for 5 minutes, to the cell suspension 800 µl LB medium are added, followed by incubation at 30 °C for 1 hour. Aliquots of the cell suspension (10 µl, 100 µl and 690 µl) are separately plated on plates of agarized (20 g/l) LB medium containing 100 µg/mg ampicillin and kept at 30 °C overnight.

40 The obtained clones (Amp<sup>R</sup>) are transferred to a nitrocellulose membrane on a LB agar plate with added ampicillin, grown at 30 °C overnight, and then tested for hybridization with three oligonucleotidic probes (UB35, UB36, UB18) terminally marked with <sup>32</sup>P having the following sequences:

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I) 5'-ATGGGTAAAGGGATTTTATC3'

II) 5'-CTATATTAGAGCCATCTTC3'

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III) 5'-TCAAAGCGCTTGACGAAG3'

55 The hybridization test is performed according to known technique. From the colonies positive to hybridization the plasmids contained in them are prepared by miniprep as described by Maniatis et al. (1982) and the ORF3D insert nucleotide sequence is controlled by known technique.

### EXAMPLE 3

Expression of the MS2-gpg3 recombination protein

*E.coli* cells containing the pEX34 vector with the ORF3D insert are inoculated in duplicate in 10 ml LB medium with added 30 µg/ml ampicillin and cultivated at 30°C overnight. The procedure described by Nicosia et al. [Inf. Imm. (1987) 55:963-967] is then followed, with the provision that one of two duplicates undergoes induction of the cloned gene by treatment at 42°C, while the other does not. Two protein extracts are thus obtained, produced by the bacterium, in 7M urea buffered at pH 8, one of which corresponds to the induced cells, and the other, as a control, to the non-induced cells.

By analysis of the protein contents of both extracts by electrophoresis in SDS-polyacrylamide 15% gel according to known techniques, it is possible to deduct the presence of a protein species of 39,000 apparent mol.wt. which is present in a considerably greater amount in the induced extracts.

In the non-induced cell lysate no evidence of such a protein, but only the product of the vector alone, is found.

Said electrophoresis patterns may be analyzed by the Western Blot technique employing a monoclonal antibody (SCLAVO) specific for the 11 kd fragment generated by the pEX34 vector. In this way it is possible to demonstrate that the 39 kd band is a fusion protein containing said fragment.

**EXAMPLE 4**Purification of MS2-gpg3 from *E.coli* K12Δ H1Δ trp extracts

The protein extract, from induced bacterial cells, re-suspended in 7M urea, is dialyzed for 15 hrs. at 4°C against a PBS buffer consisting of 0.4% KCl, 0.4% KH<sub>2</sub>PO<sub>4</sub>, 16% NaCl, 2.5% NaH<sub>2</sub>PO<sub>4</sub>.

During the dialysis a protein precipitate is obtained, which is separated by centrifuging and discarded.

The supernatant is submitted to further purification by electrophoresis on preparative 12.5% acrylamide gels, and the protein band of 39,000 mol.wt. (MS2-gpg3D) is then extracted by electroelution from the gel.

The thus obtained MS2-gpg3 is precipitated by adding to the electroeluted solution 9 volumes of absolute acetone (-20°C). The protein precipitate is separated by centrifuging, re-suspended in 90% acetone, centrifuged as above, precipitated in 96% acetone and centrifuged again. The precipitate is brought to dryness in a nitrogen stream and re-suspended in 200 µl sterile PBS at a final concentration of approximately 1.5 µg/µl.

The advantage of the effected dialysis is the elimination, with this procedure, of some *E.coli* proteins, in particular some with a molecular weight equal or very near to the one of the desired recombinant product, which may present a considerable hinderance in the electrophoretic and/or chromatographic purification.

**EXAMPLE 5**Production of polyclonal anti-MS2-pGPG3 antibodies

Utilizing the MS2-gpg3 protein, purified as in Example 4, 3 Balb/C 7-8 week old mice are immunized intraperitoneally. The immunization procedure comprises a first injection of 0.2 ml/mouse of an emulsion consisting of one part by vol. of the purified protein solution (1.5 µg/µl) and five parts of Freund complete adjuvant (FCA).

The thus inoculated protein amount is thus ca. 50 µg/mouse. After 1 week the mice are immunized with the said same emulsion, followed by a 800 µl Pristane injection. After 1 week from the second inoculation, the mice are intraperitoneally immunized with 0.2 ml of a solution similar to the first one. Finally, after two weeks from the third inoculation a booster immunization is effected. The thus induced antibodies are collected in the ascitic fluid formed after the above described treatment.

The anti MS2-gpg3 antibody titres show values comprised between 1:8000 and 1:10.000 evaluated by analysis with Western Blot containing the MS2-gpg3 protein.

The reactivity of said antibodies to the native antigen (gpg3) was evaluated according to the following methods:

- analysis with Western Blot containing total protein extracts of elemental purified CT bodies
- immunofluorescence on McCoy cells cultures infected with CT. The results of the above tests show that the anti MS2-gpg3 antibodies are able to reveal *C.trachomatis* inclusions in infected cells (see immunofluorescence test) and recognize a protein present in the bacterium protein extracts and having a mol.wt. of 28 kd, equivalent, that is, to the one of the protein encoded by ORF3D (see Western Blot test).

# EXAMPLE 6

To the end of preparing monoclonal anti-MS2-pgp3 antibodies, the mice, immunized as above described, are sacrificed, the spleens extracted and utilized for the preparation of hybridomas operating according to the technique described by Davis L.G. [Basic methods in molecular biology - Elsevier Edit., New York (1986)]. The screening of the thus obtained hybridomas is performed as described for the polyclonal antibodies. In particular, a screening was performed with induced E.coli extracts (see Example 3) containing the MS2-pgp3 protein or the polypeptide encoded by the pEX34 vector alone; obviously, the clones were selected which produced antibodies reacting only with the recombinant product. With such pgp3-specific antibodies, results are obtained which are superimposable to the ones obtained with the above described polyclonal antibodies.

# EXAMPLE 7

Serum samples from 20 patients with Chlamydia generated infections were collected. Said sera contained anti-Chlamydia antibodies with titres comprised between 128 and 512, as determined by immunofluorescence against single antigen (LGV2). 15 control sera not containing anti-Chlamydia antibodies were obtained from healthy donors. Western Blots were prepared, as above described, containing the MS2-pgp3 protein. These were incubated with the sera under examination diluted 1:100 and successively with peroxidase marked rabbit (anti human IgG) immunoglobines. 16 of the 20 infected patients sera contained antibodies apt to react with MS2-pgp3. The 15 healthy control sera did not give any reaction with said protein.

# Claims

1. pCTD plasmid isolated from Chlamydia trachomatis serotype D characterized by the following nucleotidic sequence:

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790  
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970  
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1090

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150  
210  
270  
330  
390  
450  
510  
570  
630  
690  
750  
810  
870  
930  
990  
1050  
1110

110  
170  
230  
290  
350  
410  
470  
530  
590  
650  
710  
770  
830  
890  
950  
1010  
1070  
1130

ATATT CATATTCTGTTGCCAGAAAAACACCTTTAGGCTATATTAGAGCCATCTTCTTTG  
AAGCGTTGTCTTCTCGAGAAGATTTATCGTACGCAAATATCATCTTTGCGGTTGCGTGTC  
CTGTGACCTTCATTATGTCTGGAGTCTGAGCACCCCTAGGCGTTTGTACTCCGTCACAGCGG  
TTGCTCGAAGCACGTGCGGGGTTATTTTAAAAGGGATTGCAGCTTGTAGTCCTGCTTGAG  
AGAACGTGCGGGCGATTTGCCCTTAACCCACCATTTTTCCGGAGCGAGTTACGAAGACAA  
AACCTCTTCGTTGACCGATGTACTCTTGTAGAAAGTGCATAAACTTCTGAGGATAAGTTA  
TAATAATCCTCTTTTCTGTCTGACGGTTCTTAAGCTGGGAGAAAGAAATGGTAGCTTGTT  
GGAAACAAATCTGACTAATCTCCAAGCTTAAGACTTCAGAGGAGCGTTTACCTCCTTGGA  
GCATTGTCTGGGCGATCAACCAATCCCGGGCATTGATTTTTTTTTAGCTCTTTTAGGAAGG  
ATGCTGTTTGCAAACCTGTTTCATCGCATCCGTTTTTACTATTTCCCTGGTTTTAAAAAATG  
TTCGACTATTTTCTTGTTTAGAAGGTTGCGCTATAGCGACTATTCCTTGAGTCATCCTGT  
TTAGGAATCTTGTTAAGGAAATATAGCTTGCTGCTCGAAGTTGTTTAGTACCTTCGGTCC  
AAGAAGTCTTGCGAGAGGAACTTTTTTAATCGCATCTAGGATTAGATTATGATTTAAAA  
GGGAAAACCTCTTGAGATTATATCCAAGGACAATAGACCAATCTTTCTAAAGACAAAA  
AAGATCCTCGATATGATCTACAAGTATGTTTGTTGAGTGATGCGGTCCAATGCATAATAA  
CTTCGAATAAGGAGAAGCTTTTCATGCGTTTCCAATAGGATTCTTGCGGAATTTTTAAAA  
CTTCCTGATAAGACTTTTCACTATATTCTAACGACATTTCTTGCTGCAAAGATAAAATCC  
CTTTACCCATGAAATCCCTCGTGATATAACCTATCCGTAATAATGTCCTGATTAGTGAAT  
AATCAGGTGTGAACAGGATAGCACGCTCGGTATTTTTTTATATAAACATGAAAACCTCGT

ORF1 >> MetLysThrArg

1150 1170 1190  
 5 TCCGAAATAGAAAATCGCATGCAAGATATCGAGTATGCGTTGTTAGGTAAAGCTCTGATA  
 SerGluIleGluAsnArgMetGlnAspIleGluTyrAlaLeuLeuGlyLysAlaLeuIle  
  
 1210 1230 1250  
 10 TTTGAAGACTCTACTGAGTATATTCTGAGGCAGCTTGCTAATTATGAGTTAAAGTGTCT  
 PheGluAspSerThrGluTyrIleLeuArgGlnLeuAlaAsnTyrGluPheLysCysSer  
  
 1270 1290 1310  
 CATCATAAAAACATATTCATAGTATTTAAACACTTAAAAGACAATGGATTACCTATAACT  
 HisHisLysAsnIlePheIleValPheLysHisLeuLysAspAsnGlyLeuProIleThr  
 15  
 1330 1350 1370  
 GTAGACTCGGCTTGGGAAGAGCTTTTGC GCGTCGTATCAAAGATATGGACAAATCGTAT  
 ValAspSerAlaTrpGluGluLeuLeuArgArgArgIleLysAspMetAspLysSerTyr  
  
 1390 1410 1430  
 20 CTCGGGTAAATGTTGCATGATGCTTTATCAAATGACAAGCTTAGATCCGTTTCTCATACG  
 LeuGlyLeuMetLeuHisAspAlaLeuSerAsnAspLysLeuArgSerValSerHisThr  
  
 1450 1470 1490  
 25 GTTTTCCTCGATGATTTGAGCGTGTGTAGCGCTGAAGAAAATTGAGTAATTTCAATTTTC  
 ValPheLeuAspAspLeuSerValCysSerAlaGluGluAsnLeuSerAsnPheIlePhe  
  
 1510 1530 1550  
 CGCTCGTTTAAATGAGTACAATGAAAATCCATTGCGTAGATCTCCGTTTCTATTGCTTGAG  
 ArgSerPheAsnGluTyrAsnGluAsnProLeuArgArgSerProPheLeuLeuLeuGlu  
 30  
 1570 1590 1610  
 CGTATAAAGGGAAGGCTTGATAGTGCTATAGCAAAGACTTTTTCTATTTCGCAGCGCTAGA  
 ArgIleLysGlyArgLeuAspSerAlaIleAlaLysThrPheSerIleArgSerAlaArg  
  
 1630 1650 1670  
 35 GGCCGGTCTATTTATGATATATTCTCACAGTCAGAAATTGGAGTGCTGGCTCGTATAAAA  
 GlyArgSerIleTyrAspIlePheSerGlnSerGluIleGlyValLeuAlaArgIleLys  
  
 1690 1710 1730  
 AAAAGACGAGTAGCGTTCTCTGAGAATCAAAATTCTTTCTTTGATGGCTTCCCAACAGGA  
 LysArgArgValAlaPheSerGluAsnGlnAsnSerPhePheAspGlyPheProThrGly  
 40  
 1750 1770 1790  
 TACAAGGATATTGATGATAAAGGAGTTATCTTAGCTAAAGGTAATTTCTGTGATTATAGCA  
 TyrLysAspIleAspAspLysGlyValIleLeuAlaLysGlyAsnPheValIleIleAla  
  
 1810 1830 1850  
 45 GCTAGACCATCTATAGGGAAAACAGCTTTAGCTATAGACATGGCGATAAATCTTGCGGTT  
 AlaArgProSerIleGlyLysThrAlaLeuAlaIleAspMetAlaIleAsnLeuAlaVal  
  
 1870 1890 1910  
 50 ACTCAACAGCGTAGAGTTGGTTTCTATCTCTAGAAATGAGCGCAGGTCAAATTGTTGAG  
 ThrGlnGlnArgArgValGlyPheLeuSerLeuGluMetSerAlaGlyGlnIleValGlu  
  
 1930 1950 1970  
 CGGATTATTGCTAATTTAACAGGAATATCTGGTGAAAAATTACAAAGAGGGGATCTCTCT  
 ArgIleIleAlaAsnLeuThrGlyIleSerGlyGluLysLeuGlnArgGlyAspLeuSer  
 55

1990 2010 2030  
 AAAGAAGAATTATTCGAGTAGAAGAAGCTGGAGAAACGGTTAGAGAATCACATTTTAT  
 LysGluGluLeuPheArgValGluGluAlaGlyGluThrValArgGluSerHisPheTyr  
 5  
 2050 2070 2090  
 ATCTGCAGTGATAGTCAGTATAAGCTTAACCTAATCGCGAATCAGATCCGGTTGCTGAGA  
 IleCysSerAspSerGlnTyrLysLeuAsnLeuIleAlaAsnGlnIleArgLeuLeuArg  
 10  
 2110 2130 2150  
 AAAGAAGATCGAGTAGACGTAATATTTATCGATTACTTGCAGTTGATCAACTCATCGGTT  
 LysGluAspArgValAspValIlePheIleAspTyrLeuGlnLeuIleAsnSerSerVal  
 15  
 2170 2190 2210  
 GGAGAAAATCGTCAAAAATGAAATAGCAGATATATCTAGAACCTTAAGAGGTTTAGCCTCA  
 GlyGluAsnArgGlnAsnGluIleAlaAspIleSerArgThrLeuArgGlyLeuAlaSer  
 2230 2250 2270  
 GAGCTAAACATTTCCTATAGTTTGTATCCCAACTATCTAGAAAAGTTGAGGATAGAGCA  
 GluLeuAsnIleProIleValCysLeuSerGlnLeuSerArgLysValGluAspArgAla  
 20  
 2290 2310 2330  
 AATAAAGTTCCCATGCTTTCAGATTTGCGAGACAGCGGTCAAATAGAGCAAGACGCAGAT  
 AsnLysValProMetLeuSerAspLeuArgAspSerGlyGlnIleGluGlnAspAlaAsp  
 25  
 2350 2370 2390  
 GTGATTTTGTATTCAATAGGAAGGAATCGTCTTCTAATTGTGAGATAACTGTTGGGAAA  
 ValIleLeuPheIleAsnArgLysGluSerSerSerAsnCysGluIleThrValGlyLys  
 2410 2430 2450  
 AATAGACATGGATCGGTTTTCTCTTCGGTATTACATTTTCGATCCAAAAATTAGTAAATTC  
 AsnArgHisGlySerValPheSerSerValLeuHisPheAspProLysIleSerLysPhe  
 30  
 2470 2490 2510  
 TCCGCTATTAAAAAGTATGGTAAATTATAGTAACTGCCACTTCATCAAAAGTCCTATCC  
 SerAlaIleLysLysValTrpEnd  
 ORF2 >> MetValAsnTyrSerAsnCysHisPheIleLysSerProIleH  
 35  
 2530 2550 2570  
 ACCTTGAAAATCAGAAGTTTGGAAGAAGACCTGGTCAATCTATTAAGATATCTCCCAAAT  
 isLeuGluAsnGlnLysPheGlyArgArgProGlyGlnSerIleLysIleSerProLysL  
 40  
 2590 2610 2630  
 TGGCTCAAAATGGGATGGTAGAAGTTATAGGTCTTGATTTTCTTTCATCTCATTACCATG  
 euAlaGlnAsnGlyMetValGluValIleGlyLeuAspPheLeuSerSerHisTyrHisA  
 2650 2670 2690  
 CATTAGCAGCTATCCAAAGATTACTGACCGCAACGAATTACAAGGGGAACACAAAAGGGG  
 laLeuAlaAlaIleGlnArgLeuLeuThrAlaThrAsnTyrLysGlyAsnThrLysGlyV  
 45  
 2710 2730 2750  
 TTGTTTTATCCAGAGAATCAAATAGTTTTCAATTTGAAGGATGGATACCAAGAATCCGTT  
 alValLeuSerArgGluSerAsnSerPheGlnPheGluGlyTrpIleProArgIleArgP  
 50  
 2770 2790 2810  
 TTACAAAACCTGAATTCTTAGAGGCTTATGGAGTTAAGCGGTATAAACATCCAGAAATA  
 heThrLysThrGluPheLeuGluAlaTyrGlyValLysArgTyrLysThrSerArgAsnL  
 55

2830 2850 2870  
 AGTATGAGTTTAGTGGAAGAAGCTGAACTGCTTTAGAAAGCCTTATACCATTTAGGAC  
 ysTyrGluPheSerGlyLysGluAlaGluThrAlaLeuGluAlaLeuTyrHisLeuGlyH  
 5 2890 2910 2930  
 ATCAACCGTTTTTAATAGTGGAAGCTGAACTCGATGGACTAATGGAACACAAATAGTAG  
 isGlnPropPheLeuIleValAlaThrArgThrArgTrpThrAsnGlyThrGlnIleValA  
 10 2950 2970 2990  
 ACCGTTACCAAACCTCTTTCTCCGATCATTAGGATTTACGAAGGATGGGAAGGTTTAACTG  
 spArgTyrGlnThrLeuSerProIleIleArgIleTyrGluGlyTrpGluGlyLeuThrA  
 15 3010 3030 3050  
 ACGAAGAAAATATAGATATAGACTTAACACCTTTTAATTCACCACCTACACGGAACATA  
 spGluGluAsnIleAspIleAspLeuThrProPheAsnSerProProThrArgLysHisL  
 20 3070 3090 3110  
 AAGGGTTTCGTTGTAGAGCCATGTCCTATCTTGGTAGATCAAATAGAATCCTACTTTGTAA  
 ysGlyPheValValGluProCysProIleLeuValAspGlnIleGluSerTyrPheValI  
 25 3130 3150 3170  
 TCAAGCCTGCAAATGTATACCAAGAAATAAAATGCGTTTCCCAAATGCATCAAAGTATG  
 leLysProAlaAsnValTyrGlnGluIleLysMetArgPheProAsnAlaSerLysTyrA  
 3190 3210 3230  
 CTTACACATTTATCGACTGGGTGATTACAGCAGCTGCGAAAAAGAGACGAAAATTAAC  
 laTyrThrPheIleAspTrpValIleThrAlaAlaAlaLysLysArgArgLysLeuThrL  
 3250 3270 3290  
 AGGATAATTCTTGCCAGAAAACCTGTTATTAAACGTTAACGTTAAAAGTCTTGCATATA  
 ysAspAsnSerTrpProGluAsnLeuLeuLeuAsnValAsnValLysSerLeuAlaTyrI  
 30 3310 3330 3350  
 TTTTAAGGATGAATCGGTACATCTGTACAAGGAAGTGGAAAAAATCGAGTTAGCTATCG  
 leLeuArgMetAsnArgTyrIleCysThrArgAsnTrpLysLysIleGluLeuAlaIleA  
 35 3370 3390 3410  
 ATAAATGTATAGAAATCGCCATTCTAGCTTGGCTGGTTATCTAGAAAGAAACGCATTGAAT  
 spLysCysIleGluIleAlaIleGlnLeuGlyTrpLeuSerArgArgLysArgIleGluP  
 40 3430 3450 3470  
 TTCTGGATTCTTCTAAACTCTCTAAAAAGAAATTCTATATCTAAATAAGAGCGCTTTG  
 heLeuAspSerSerLysLeuSerLysLysGluIleLeuTyrLeuAsnLysGluArgPheG  
 3490 3510 3530  
 AAGAAATAACTAAGAAATCTAAAGAACAAATGGAACAATTAGAACAAGAATCTATTAATT  
 luGluIleThrLysLysSerLysGluGlnMetGluGlnLeuGluGlnGluSerIleAsnE  
 45 3550 3570 3590  
 AATAGCAAGCTTGAACTAAAAACCTAATTTATTTAAAGCTCAAAATAAAAAAGAGTTTT  
 nd  
 50 3610 3630 3650  
 AAAATGGGAAATTCTGGTTTTTATTTGTATAACACTGAAACTGCGTCTTTGCTGATAAT  
 ORF3>> MetGlyAsnSerGlyPheTyrLeuTyrAsnThrGluAsnCysValPheAlaAspAsn  
 55 3670 3690 3710  
 ATCAAAGTTGGGCAAATGACAGAGCCGCTCAAGGACCAGCAAATAATCCTTGGGACAACA  
 IleLysValGlyGlnMetThrGluProLeuLysAspGlnGlnIleIleLeuGlyThrThr

3730 3750 3770  
 TCAACACCTGTCGCAGCCAAAATGACAGCTTCTGATGGAATATCTTTAACAGTCTCCAAT  
 SerThrProValAlaAlaLysMetThrAlaSerAspGlyIleSerLeuThrValSerAsn  
 5 3790 3810 3830  
 AATTCATCAACCAATGCTTCTATTACAATTGGTTTGGATGCGGAAAAAGCTTACCAGCTT  
 AsnSerSerThrAsnAlaSerIleThrIleGlyLeuAspAlaGluLysAlaTyrGlnLeu  
 10 3850 3870 3890  
 ATTCTAGAAAAGTTGGGAGATCAAATTCCTTGATGGAATTGCTGATACTATTGTTGATAGT  
 IleLeuGluLysLeuGlyAspGlnIleLeuAspGlyIleAlaAspThrIleValAspSer  
 15 3910 3930 3950  
 ACAGTCCAAGATATTTTAGACAAAATCAAAACAGACCCTTCTCTAGGTTTGTGAAAGCT  
 ThrValGlnAspIleLeuAspLysIleLysThrAspProSerLeuGlyLeuLeuLysAla  
 20 3970 3990 4010  
 TTTAACAACCTTTCCAATCACTAATAAAATTCAATGCAACGGGTATTCACTCCCAGTAAC  
 PheAsnAsnPheProIleThrAsnLysIleGlnCysAsnGlyLeuPheThrProSerAsn  
 25 4030 4050 4070  
 ATTGAAACTTTATTAGGAGGAACTGAAATAGGAAAATTCACAGTCACACCCAAAAGCTCT  
 IleGluThrLeuLeuGlyGlyThrGluIleGlyLysPheThrValThrProLysSerSer  
 30 4090 4110 4130  
 GGGAGCATGTTCTTAGTCTCAGCAGATATTATTGCATCAAGAATGGAAGGCGGCTTGTT  
 GlySerMetPheLeuValSerAlaAspIleIleAlaSerArgMetGluGlyGlyValVal  
 35 4150 4170 4190  
 CTAGCTTTGGTACGAGAAGGTGATTCTAAGCCCTGCGCGATTAGTTATGGATACTCATCA  
 LeuAlaLeuValArgGluGlyAspSerLysProCysAlaIleSerTyrGlyTyrSerSer  
 40 4210 4230 4250  
 GGCATTCTTAATTTATGTAGTCTAAGAACCAGTATTACTAATACAGGATTGACTCCGACA  
 GlyIleProAsnLeuCysSerLeuArgThrSerIleThrAsnThrGlyLeuThrProThr  
 45 4270 4290 4310  
 ACGTATTTCATTACGTGTAGGCGGTTTAGAAAGCGGTGTGGTATGGGTAAATGCCCTTTCT  
 ThrTyrSerLeuArgValGlyGlyLeuGluSerGlyValValTrpValAsnAlaLeuSer  
 50 4330 4350 4370  
 AATGGCAATGATATTTTAGGAATAACAAATACTTCTAATGTATCTTTTTTAGAGGTAATA  
 AsnGlyAsnAspIleLeuGlyIleThrAsnThrSerAsnValSerPheLeuGluValIle  
 4390 4410 4430  
 CCTCAAACAAACGCTTAAACAAATTTTTATTGGATTTTTCTTATAGGTTTTATTTAGAG  
 ProGlnThrAsnAlaEnd  
 45 4450 4470 4490  
 AAAACAGTTCGAATTACGGGGTTTGTTATGCAAAATAAAAGAAAAGTGAGGGACGATTTT  
 ORF4 >> MetGlnAsnLysArgLysValArgAspAspPhe  
 50 4510 4530 4550  
 ATTAATAATTGTTAAAGATGTGAAAAAGATTTCCCGAATTAGACCTAAAAATACGAGTA  
 IleLysIleValLysAspValLysLysAspPheProGluLeuAspLeuLysIleArgVal  
 55 4570 4590 4610  
 AACAAGGAAAAAGTAACTTTCTTAAATCTCCCTTAGAACTCTACCATAAAAGTGTCTCA  
 AsnLysGluLysValThrPheLeuAsnSerProLeuGluLeuTyrHisLysSerValSer

4630 4650 4670  
 CTAATTCTAGGACTGCTTCAACAAATAGAAAACCTCTTTAGGATTATTCCCAGACTCTCCT  
 5 LeuIleLeuGlyLeuLeuGlnGlnIleGluAsnSerLeuGlyLeuPheProAspSerPro

4690 4710 4730  
 GTTCTTGAAAAATTAGAGGATAACAGTTTAAAGCTAAAAAAGGCTTTGATTATGCTTATC  
 10 ValLeuGluLysLeuGluAspAsnSerLeuLysLeuLysLysAlaLeuIleMetLeuIle

4750 4770 4790  
 TTGTCTAGAAAAGACATGTTTTCCAAGGCTGAATAGACAACTTACTCTAACGTTGGAGTT  
 LeuSerArgLysAspMetPheSerLysAlaGluEnd

4810 4830 4850  
 15 ORF5 >> GATTTGCACACCTTAGTTTTTGTCTCTTTTAAGGGAGGAACTGGAAAAACAACACTTTCT  
 LeuHisThrLeuValPheCysSerPheLysGlyGlyThrGlyLysThrThrLeuSer

4870 4890 4910  
 CTAACGTGGGATGCAACTTGGCCCAATTTTATAGGGAAAAAAGTGTACTTGTGACCTA  
 LeuAsnValGlyCysAsnLeuAlaGlnPheLeuGlyLysLysValLeuLeuAlaAspLeu

4930 4950 4970  
 20 GACCCGCAATCCAATTTATCTTCTGGATTGGGGGCTAGTGTGAGAAGTGACCAAAAAGGC  
 AspProGlnSerAsnLeuSerSerGlyLeuGlyAlaSerValArgSerAspGlnLysGly

4990 5010 5030  
 25 TTGCACGACATAGTATACACATCAAACGATTTAAATCAATCATTTGCGAAACAAAAAA  
 LeuHisAspIleValTyrThrSerAsnAspLeuLysSerIleIleCysGluThrLysLys

5050 5070 5090  
 30 GATAGTGTGGACCTAATTCCTGCATCATTTTCATCCGAACAGTTTAGAGAATTGGATATT  
 AspSerValAspLeuIleProAlaSerPheSerSerGluGlnPheArgGluLeuAspIle

5110 5130 5150  
 CATAGAGGACCTAGTAACAACCTAAAGTTATTTCTGAATGAGTACTGCGCTCCTTTTTAT  
 HisArgGlyProSerAsnAsnLeuLysLeuPheLeuAsnGluTyrCysAlaProPheTyr

5170 5190 5210  
 35 GACATCTGCATAATAGACACTCCACCTAGCCTAGGAGGGTTAACGAAAGAAGCTTTTGT  
 AspIleCysIleIleAspThrProProSerLeuGlyGlyLeuThrLysGluAlaPheVal

5230 5250 5270  
 40 GCAGGAGACAAATTAATTGCTTGTTTAACTCCAGAACCTTTTTCTATTCTAGGGTTACAA  
 AlaGlyAspLysLeuIleAlaCysLeuThrProGluProPheSerIleLeuGlyLeuGln

5290 5310 5330  
 AAGATACGTGAATTCTTAAGTTCGGTCGGAAAACCTGAAGAAGAACACATTCTTGAATA  
 LysIleArgGluPheLeuSerSerValGlyLysProGluGluGluHisIleLeuGlyIle

5350 5370 5390  
 45 GCTTTGTCTTTTTGGGATGATCGTAACCTCGACTAACCAAATGTATATAGACATTATCGAG  
 AlaLeuSerPheTrpAspAspArgAsnSerThrAsnGlnMetTyrIleAspIleIleGlu

5410 5430 5450  
 50 TCTATTTACAAAAACAAGCTTTTTTCAACAAAAATTCGTCGAGATATTTCTCTCAGCCGT  
 SerIleTyrLysAsnLysLeuPheSerThrLysIleArgArgAspIleSerLeuSerArg

5470 5490 5510  
 55 TCTCTTCTTAAAGAAGATTCTGTAGCTAATGTCTATCCAAATTCTAGGGCCGCAGAAGAT  
 SerLeuLeuLysGluAspSerValAlaAsnValTyrProAsnSerArgAlaAlaGluAsp

5530 5550 5570  
 5 ATTCTGAAGTTAACGCATGAAATAGCAAATATTTTGCATATCGAATATGAACGAGATTAC  
 IleLeuLysLeuThrHisGluIleAlaAsnIleLeuHisIleGluTyrGluArgAspTyr  
  
 5590 5610 5630  
 10 TCTCAGAGGACAACGTGAACAACTAAAAAAGAAGCGGATGTCTTTTTTAAAAAAAATC  
 SerGlnArgThrThrEnd  
 ORF6 >> ValAsnLysLeuLysLysGluAlaAspValPhePheLysLysAsnG  
  
 5650 5670 5690  
 15 AAAGTCCGCTTCTCTAGATTTTAAGAAGACGCTTCCCTCCATTGAAGTATTCTCAGCAA  
 lnThrAlaAlaSerLeuAspPheLysLysThrLeuProSerIleGluLeuPheSerAlaT  
  
 5710 5730 5750  
 CTTTGAATTCTGAGGAAAGTCAGAGTTTGGATCGATTATTTTTATCAGAGTCCCAAACT  
 hrLeuAsnSerGluGluSerGlnSerLeuAspArgLeuPheLeuSerGluSerGlnAsnT  
  
 5770 5790 5810  
 20 ATTCCGATGAAGAATTTTATCAAGAAGACATCCTAGCGGTAAACTGCTTACTGGTCAGA  
 yrSerAspGluGluPheTyrGlnGluAspIleLeuAlaValLysLeuLeuThrGlyGlnI  
  
 5830 5850 5870  
 25 TAAAATCCATACAGAAGCAACACGTACTTCTTTTAGGAGAAAAATCTATAATGCTAGAA  
 leLysSerIleGlnLysGlnHisValLeuLeuLeuGlyGluLysIleTyrAsnAlaArgL  
  
 5890 5910 5930  
 30 AAATCCTGAGTAAGGATCACTTCTCCTCAACAACCTTTTTCATCTTGGATAGAGTTAGTTT  
 ysIleLeuSerLysAspHisPheSerSerThrThrPheSerSerTrpIleGluLeuValP  
  
 5950 5970 5990  
 TTAGAACTAAGTCTTCTGCTTACAATGCTCTTGCATATTACGAGCTTTTTATAAACCTCC  
 heArgThrLysSerSerAlaTyrAsnAlaLeuAlaTyrTyrGluLeuPheIleAsnLeuP  
  
 6010 6030 6050  
 35 CCAACCAAACCTCTACAAAAGAGTTTCAATCGATCCCCTATAAATCCGCATATATTTTGG  
 roAsnGlnThrLeuGlnLysGluPheGlnSerIleProTyrLysSerAlaTyrIleLeuA  
  
 6070 6090 6110  
 40 CCGCTAGAAAAGGCGATTAAAAACCAAGGTCGATGTGATAGGGAAAGTATGTGGAATGT  
 laAlaArgLysGlyAspLeuLysThrLysValAspValIleGlyLysValCysGlyMetS  
  
 6130 6150 6170  
 45 CGAACTCATCGGCGATAAGGGTGTGGATCAATTTCTTCCTTCATCTAGAAACAAAGACG  
 erAsnSerSerAlaIleArgValLeuAspGlnPheLeuProSerSerArgAsnLysAspV  
  
 6190 6210 6230  
 TTAGAGAAACGATAGATAAGTCTGATTAGAGAAGAATCGCCAATTATCTGATTTCTTAA  
 alArgGluThrIleAspLysSerAspSerGluLysAsnArgGlnLeuSerAspPheLeuI  
  
 6250 6270 6290  
 50 TAGAGATACTTCGCATCATGTGTTCCGGAGTTTCTTTGTCTCCTATAACGAAAATCTTC  
 leGluIleLeuArgIleMetCysSerGlyValSerLeuSerSerTyrAsnGluAsnLeuL  
  
 6310 6330 6350  
 55 TACAACAGCTTTTTGAACTTTTAAGCAAAAGAGCTGATCCTCCGTACGCTCATATATAT  
 euGlnGlnLeuPheGluLeuPheLysGlnLysSerEnd

5           6370                           6390                           6410  
 ATATCTATTATATATATATATTTAGGGATTGATTTACGAGAGAGATTGCAACTCTTG  
  
           6430                           6450                           6470  
 GTGGTAGACTTTGCAACTCTTGGTGGTAGACTTTGCAACTCTTGGTGGTAGACTTTGCAA  
  
 10          6490                           6510                           6530  
 CTCTTGGTGGTAGACTTGGTCATAATGGACTTTTGTTAAAAAATTTATTAAATCTTAGA  
  
           6550                           6570                           6590  
 GCTCCGATTTTGAATAGCTTTGGTTAAGAAAATGGGCTCGATGGCTTTCCATAAAAGTAG  
 ORF7 >> LeuValLysLysMetGlySerMetAlaPheHisLysSerAr  
  
 15          6610                           6630                           6650  
 ATTGTTTTTAACTTTTGGGGACGCGTCGGAAATTTGGTTATCTACTTTATCTTATCTAAC  
 gLeuPheLeuThrPheGlyAspAlaSerGluIleTrpLeuSerThrLeuSerTyrLeuTh  
  
 20          6670                           6690                           6710  
 TAGAAAAAATTATGCGTCTGGGATTAACTTTCTTGTCTTTAGAGATTCTGGATTTATC  
 rArgLysAsnTyrAlaSerGlyIleAsnPheLeuValSerLeuGluIleLeuAspLeuSe  
  
 25          6730                           6750                           6770  
 GGAAACCTTGATAAAGGCTATTTCTCTTGACCACAGCGAATCTTTGTTTTAAATCAAGTC  
 rGluThrLeuIleLysAlaIleSerLeuAspHisSerGluSerLeuPheLysIleLysSe  
  
 30          6790                           6810                           6830  
 TCTAGATGTTTTTAATGGAAAAGTTGTTTCAGAGGCATCTAAACAGGCTAGAGCGGCATG  
 rLeuAspValPheAsnGlyLysValValSerGluAlaSerLysGlnAlaArgAlaAlaCy  
  
 35          6850                           6870                           6890  
 CTACATCTTTTCAAAAGTTTTTGTATAGATTGACCAAGGGATATATTAAACCCGCTAT  
 sTyrIleSerPheThrLysPheLeuTyrArgLeuThrLysGlyTyrIleLysProAlaIl  
  
 40          6910                           6930                           6950  
 TCCATTGAAAGATTTTGGAAACACTACATTTTTTAAAAATCCGAGACAAAATCAAAACAGA  
 eProLeuLysAspPheGlyAsnThrThrPhePheLysIleArgAspLysIleLysThrGl  
  
 45          6970                           6990                           7010  
 ATCGATTTCTAAGCAGGAATGGACAGTTTTTTTTGAAGCGCTCCGGATAGTGAATTATAG  
 uSerIleSerLysGlnGluTrpThrValPhePheGluAlaLeuArgIleValAsnTyrAr  
  
 50          7030                           7050                           7070  
 AGACTATTTAATCGGTAAATTGATTGTACAAGGGATCCGTAAGTTAGACGAAATTTTGTC  
 gAspTyrLeuIleGlyLysLeuIleValGlnGlyIleArgLysLeuAspGluIleLeuSe  
  
 55          7090                           7110                           7130  
 TTTGCGCACAGACGATCTATTTTTTGCATCCAATCAGATTTCTTTTCGCATTAAAAAAG  
 rLeuArgThrAspAspLeuPhePheAlaSerAsnGlnIleSerPheArgIleLysLysAr  
  
           7150                           7170                           7190  
 ACAGAATAAAGAAACCAAAATTCTAATCACATTTCTATCAGCTTAATGGAAGAGTTGCA  
 gGlnAsnLysGluThrLysIleLeuIleThrPheProIleSerLeuMetGluGluLeuGl  
  
           7210                           7230                           7250  
 AAAATACACTTGTGGGAGAAATGGGAGAGTATTTGTTTCTAAAATAGGGATTCTGTAAAC  
 nLysTyrThrCysGlyArgAsnGlyArgValPheValSerLysIleGlyIleProValTh

7270                      7290                      7310  
 5 AACAAAGTCAGGTTGCGCATAATTTTAGGCTTGCAGAGTCCATAGTGCTATGAAAATAAA  
 rThrSerGlnValAlaHisAsnPheArgLeuAlaGluPheHisSerAlaMetLysIleLy  
  
 7330                      7350                      7370  
 10 AATTACTCCCAGAGTACTTCGTGCAAGCGCTTTGATTCATTTAAAGCAAATAGGATTAAA  
 sIleThrProArgValLeuArgAlaSerAlaLeuIleHisLeuLysGlnIleGlyLeuLy  
  
 7390                      7410                      7430  
 AGATGAGGAAATCATGCGTATTTCTCTGCTTTTCATCGAGACAAAGTGTGTGTTCTTATTG  
 sAspGluGluIleMetArgIleSerCysLeuSerSerArgGlnSerValCysSerTyrCy  
  
 15 7450                      7470                      7490  
 TTCTGGGGAAGAGGTAATTCCTCTAGTACAAACACCCACAATATTGTGATATAATTAAAA  
 sSerGlyGluGluValIleProLeuValGlnThrProThrIleLeuEnd

20 TT

- 25 2. pGO plasmid constituted by the pUC8 recombinant plasmid containing an insert corresponding to the nucleotidic sequence as per claim 1, cloned in the Bam H1 site.
3. Escherichia coli transformed with the plasmid according to claim 2 and deposited as ATCC 68314.
- 30 4. ORF1D gene characterized by the nucleotidic sequence comprised between 1129 and 2481 in the nucleotidic sequence according to claim 1.
5. ORF2D gene characterized by the nucleotidic sequence comprised between 2480 and 3539 in the nucleotidic sequence according to claim 1.
- 35 6. ORF3D gene characterized by the nucleotidic sequence comprised between 3604 and 4395 in the nucleotidic sequence according to claim 1.
7. ORF4D gene characterized by the nucleotidic sequence comprised between 4468 and 4773 in the nucleotidic sequence according to claim 1.
- 40 8. ORF5D gene characterized by the nucleotidic sequence comprised between 4804 and 5595 in the nucleotidic sequence according to claim 1.
9. ORF6D gene characterized by the nucleotidic sequence comprised between 5595 and 6335 in the nucleotidic sequence according to claim 1.
- 45 10. ORF7D gene characterized by the nucleotidic sequence comprised between 6560 and 7486 in the nucleotidic sequence according to claim 1.
- 50 11. ORF8D gene characterized by the nucleotidic sequence complementary to the one comprised between 41 and 1030 in the nucleotidic sequence according to claim 1.
12. Protein expressed by the gene according to claim 4 and characterized by the following aminoacid sequence:

55

pgpl:

5 MetLysThrArgSerGluIleGluAsnArgMetGlnAspIleGluTyrAlaLeuLeuGly  
 LysAlaLeuIlePheGluAspSerThrGluTyrIleLeuArgGlnLeuAlaAsnTyrGlu  
 PheLysCysSerHisHisLysAsnIlePheIleValPheLysHisLeuLysAspAsnGly  
 10 LeuProIleThrValAspSerAlaTrpGluGluLeuLeuArgArgArgIleLysAspMet  
 AspLysSerTyrLeuGlyLeuMetLeuHisAspAlaLeuSerAsnAspLysLeuArgSer  
 ValSerHisThrValPheLeuAspAspLeuSerValCysSerAlaGluGluAsnLeuSer  
 15 AsnPheIlePheArgSerPheAsnGluTyrAsnGluAsnProLeuArgArgSerProPhe  
 LeuLeuLeuGluGlyArgSerIleTyrAspIlePheSerGlnSerGluIleGlyValLeu  
 20 AlaArgIleLysLysArgArgValAlaPheSerGluAsnGlnAsnSerPhePheAspGly  
 PheProThrGlyTyrLysAspIleAspAspLysGlyValIleLeuAlaLysGlyAsnPhe  
 ValIleIleAlaAlaArgProSerIleGlyLysThrAlaLeuAlaIleAspMetAlaIle  
 25 AsnLeuAlaValThrGlnGlnArgArgValGlyPheLeuSerLeuGluMetSerAlaGly  
 GlnIleValGluArgIleIleAlaAsnLeuThrGlyIleSerGlyGluLysLeuGlnArg  
 30  
 GlyAspLeuSerLysGluGluLeuPheArgValGluGluAlaGlyGluThrValArgGlu  
 35 SerHisPheTyrIleCysSerAspSerGlnTyrLysLeuAsnLeuIleAlaAsnGlnIle  
 ArgLeuLeuArgLysGluAspArgValAspValIlePheIleAspTyrLeuGlnLeuIle  
 AsnSerSerValGlyGluAsnArgGlnAsnGluIleAlaAspIleSerArgThrLeuArg  
 40 GlyLeuAlaSerGluLeuAsnIleProIleValCysLeuSerGlnLeuSerArgLysVal  
 GluAspArgAlaAsnLysValProMetLeuSerAspLeuArgAspSerGlyGlnIleGlu  
 GlnAspAlaAspValIleLeuPheIleAsnArgLysGluSerSerSerAsnCysGluIle  
 45 ThrValGlyLysAsnArgHisGlySerValPheSerSerValLeuHisPheAspProLys  
 IleSerLysPheSerAlaIleLysLysValTrpEnd

50 or parts of it.

13. Protein expressed by the gene according to claim 5 and characterized by the following aminoacid sequence:

55

pgp2 :

MetValAsnTyrSerAsnCysHisPheIleLysSerProIleHisLeuGluAsnGlnLys  
 5 PheGlyArgArgProGlyGlnSerIleLysIleSerProLysLeuAlaGlnAsnGlyMet  
 ValGluValIleGlyLeuAspPheLeuSerSerHisTyrHisAlaLeuAlaAlaIleGln  
 10 ArgLeuLeuThrAlaThrAsnTyrLysGlyAsnThrLysGlyValValLeuSerArgGlu  
 SerAsnSerPheGlnPheGluGlyTrpIleProArgIleArgPheThrLysThrGluPhe  
 LeuGluAlaTyrGlyValLysArgTyrLysThrSerArgAsnLysTyrGluPheSerGly  
 15 LysGluAlaGluThrAlaLeuGluAlaLeuTyrHisLeuGlyHisGlnProPheLeuIle  
 ValAlaThrArgThrArgTrpThrAsnGlyThrGlnIleValAspArgTyrGlnThrLeu  
 SerProIleIleArgIleTyrGluGlyTrpGluGlyLeuThrAspGluGluAsnIleAsp  
 20 IleAspLeuThrProPheAsnSerProProThrArgLysHisLysGlyPheValValGlu  
 ProCysProIleLeuValAspGlnIleGluSerTyrPheValIleLysProAlaAsnVal  
 TyrGlnGluIleLysMetArgPheProAsnAlaSerLysTyrAlaTyrThrPheIleAsp  
 25 TrpValIleThrAlaAlaAlaLysLysArgArgLysLeuThrLysAspAsnSerTrpPro  
 GluAsnLeuLeuLeuAsnValAsnValLysSerLeuAlaTyrIleLeuArgMetAsnArg  
 TyrIleCysThrArgAsnTrpLysLysIleGluLeuAlaIleAspLysCysIleGluIle  
 30 AlaIleGlnLeuGlyTrpLeuSerArgArgLysArgIleGluPheLeuAspSerSerLys  
 35 LeuSerLysLysGluIleLeuTyrLeuAsnLysGluArgPheGluGluIleThrLysLys  
 SerLysGluGlnMetGluGlnLeuGluGlnGluSerIleAsnEnd

40 or parts of it.

14. Protein expressed by the gene according to claim 6 and characterized by the following aminoacid  
 45 sequence:

50

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pgp3:

MetGlyAsnSerGlyPheTyrLeuTyrAsnThrGluAsnCysValPheAlaAspAsnIle  
 5 LysValGlyGlnMetThrGluProLeuLysAspGlnGlnIleIleLeuGlyThrThrSer  
 ThrProValAlaAlaLysMetThrAlaSerAspGlyIleSerLeuThrValSerAsnAsn  
 SerSerThrAsnAlaSerIleThrIleGlyLeuAspAlaGluLysAlaTyrGlnLeuIle  
 10 LeuGluLysLeuGlyAspGlnIleLeuAspGlyIleAlaAspThrIleValAspSerThr  
 ValGlnAspIleLeuAspLysIleLysThrAspProSerLeuGlyLeuLeuLysAlaPhe  
 AsnAsnPheProIleThrAsnLysIleGlnCysAsnGlyLeuPheThrProSerAsnIle  
 15 GluThrLeuLeuGlyGlyThrGluIleGlyLysPheThrValThrProLysSerSerGly  
 SerMetPheLeuValSerAlaAspIleIleAlaSerArgMetGluGlyGlyValValLeu  
 20 AlaLeuValArgGluGlyAspSerLysProCysAlaIleSerTyrGlyTyrSerSerGly  
 IleProAsnLeuCysSerLeuArgThrSerIleThrAsnThrGlyLeuThrProThrThr  
 TyrSerLeuArgValGlyGlyLeuGluSerGlyValValTrpValAsnAlaLeuSerAsn  
 25 GlyAsnAspIleLeuGlyIleThrAsnThrSerAsnValSerPheLeuGluValIlePro  
 GlnThrAsnAlaEnd

30 or parts of it.

15. Protein expressed by the gene according to claim 7 and characterized by the following aminoacid sequence:

35

pgp4:

MetGlnAsnLysArgLysValArgAspAspPheIleLysIleValLysAspValLysLys  
 40 AspPheProGluLeuAspLeuLysIleArgValAsnLysGluLysValThrPheLeuAsn  
 SerProLeuGluLeuTyrHisLysSerValSerLeuIleLeuGlyLeuLeuGlnGlnIle  
 GluAsnSerLeuGlyLeuPheProAspSerProValLeuGluLysLeuGluAspAsnSer  
 45 LeuLysLeuLysLysAlaLeuIleMetLeuIleLeuSerArgLysAspMetPheSerLys  
 AlaGluEnd

50 or parts of it.

16. Protein expressed by the gene according to claim 8 and characterized by the following aminoacid sequence:

55

pgp5:

LeuHisThrLeuValPheCysSerPheLysGlyGlyThrGlyLysThrThrLeuSerLeu  
 5 AsnValGlyCysAsnLeuAlaGlnPheLeuGlyLysLysValLeuLeuAlaAspLeuAsp  
 ProGlnSerAsnLeuSerSerGlyLeuGlyAlaSerValArgSerAspGlnLysGlyLeu  
 10 HisAspIleValTyrThrSerAsnAspLeuLysSerIleIleCysGluThrLysLysAsp  
 SerValAspLeuIleProAlaSerPheSerSerGluGlnPheArgGluLeuAspIleHis  
 ArgGlyProSerAsnAsnLeuLysLeuPheLeuAsnGluTyrCysAlaProPheTyrAsp  
 15 IleCysIleIleAspThrProProSerLeuGlyGlyLeuThrLysGluAlaPheValAla  
 GlyAspLysLeuIleAlaCysLeuThrProGluProPheSerIleLeuGlyLeuGlnLys  
 IleArgGluPheLeuSerSerValGlyLysProGluGluGluHisIleLeuGlyIleAla  
 20 LeuSerPheTrpAspAspArgAsnSerThrAsnGlnMetTyrIleAspIleIleGluSer  
 IleTyrLysAsnLysLeuPheSerThrLysIleArgArgAspIleSerLeuSerArgSer  
 25 LeuLeuLysGluAspSerValAlaAsnValTyrProAsnSerArgAlaAlaGluAspIle  
 LeuLysLeuThrHisGluIleAlaAsnIleLeuHisIleGluTyrGluArgAspTyrSer  
 30 GlnArgThrThrEnd

or parts of it.

17. Protein expressed by the gene according to claim 9 and characterized by the following aminoacid  
 35 sequence:

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pgp6:

ValAsnLysLeuLysLysGluAlaAspValPhePheLysLysAsnGlnThrAlaAlaSer  
 5 LeuAspPheLysLysThrLeuProSerIleGluLeuPheSerAlaThrLeuAsnSerGlu  
 GluSerGlnSerLeuAspArgLeuPheLeuSerGluSerGlnAsnTyrSerAspGluGlu  
 10 PheTyrGlnGluAspIleLeuAlaValLysLeuLeuThrGlyGlnIleLysSerIleGln  
 LysGlnHisValLeuLeuLeuGlyGluLysIleTyrAsnAlaArgLysIleLeuSerLys  
 AspHisPheSerSerThrThrPheSerSerTrpIleGluLeuValPheArgThrLysSer  
 15 SerAlaTyrAsnAlaLeuAlaTyrTyrGluLeuPheIleAsnLeuProAsnGlnThrLeu  
 GlnLysGluPheGlnSerIleProTyrLysSerAlaTyrIleLeuAlaAlaArgLysGly  
 AspLeuLysThrLysValAspValIleGlyLysValCysGlyMetSerAsnSerSerAla  
 20 IleArgValLeuAspGlnPheLeuProSerSerArgAsnLysAspValArgGluThrIle  
 AspLysSerAspSerGluLysAsnArgGlnLeuSerAspPheLeuIleGluIleLeuArg  
 25 IleMetCysSerGlyValSerLeuSerSerTyrAsnGluAsnLeuLeuGlnGlnLeuPhe  
 GluLeuPheLysGlnLysSerEnd

or parts of it.

30

18. Protein expressed by the gene according to claim 10 and characterized by the following aminoacid sequence:

pgp7 :

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LeuValLysLysMetGlySerMetAlaPheHisLysSerArgLeuPheLeuThrPheGly  
 AspAlaSerGluIleTrpLeuSerThrLeuSerTyrLeuThrArgLysAsnTyrAlaSer  
 40 GlyIleAsnPheLeuValSerLeuGluIleLeuAspLeuSerGluThrLeuIleLysAla  
 IleSerLeuAspHisSerGluSerLeuPheLysIleLysSerLeuAspValPheAsnGly

45

50

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LysValValSerGluAlaSerLysGlnAlaArgAlaAlaCysTyrIleSerPheThrLys  
 PheLeuTyrArgLeuThrLysGlyTyrIleLysProAlaIleProLeuLysAspPheGly  
 5 AsnThrThrPhePheLysIleArgAspLysIleLysThrGluSerIleSerLysGlnGlu  
 TrpThrValPhePheGluAlaLeuArgIleValAsnTyrArgAspTyrLeuIleGlyLys  
 LeuIleValGlnGlyIleArgLysLeuAspGluIleLeuSerLeuArgThrAspAspLeu  
 10 PhePheAlaSerAsnGlnIleSerPheArgIleLysLysArgGlnAsnLysGluThrLys  
 IleLeuIleThrPheProIleSerLeuMetGluGluLeuGlnLysTyrThrCysGlyArg  
 AsnGlyArgValPheValSerLysIleGlyIleProValThrThrSerGlnValAlaHis  
 15 AsnPheArgLeuAlaGluPheHisSerAlaMetLysIleLysIleThrProArgValLeu  
 ArgAlaSerAlaLeuIleHisLeuLysGlnIleGlyLeuLysAspGluGluIleMetArg  
 20 IleSerCysLeuSerSerArgGlnSerValCysSerTyrCysSerGlyGluGluValIle  
 ProLeuValGlnThrProThrIleLeuEnd

or parts of it.

19. Protein expressed by the gene according to claim 11 and characterized by the following aminoacid sequence:

pgp8 :

MetGlyLysGlyIleLeuSerLeuGlnGlnGluMetSerLeuGluTyrSerGluLysSer  
 35 TyrGlnGluValLeuLysIleArgGlnGluSerTyrTrpLysArgMetLysSerPheSer  
 LeuPheGluValIleMetHisTrpThrAlaSerLeuAsnLysHisThrCysArgSerTyr  
 ArgGlySerPheLeuSerLeuGluLysIleGlyLeuLeuSerLeuAspMetAsnLeuGln  
 40 GluPheSerLeuLeuAsnHisAsnLeuIleLeuAspAlaIleLysLysValSerSerAla  
 LysThrSerTrpThrGluGlyThrLysGlnValArgAlaAlaSerTyrIleSerLeuThr  
 ArgPheLeuAsnArgMetThrGlnGlyIleValAlaIleAlaGlnProSerLysGlnGlu  
 45 AsnSerArgThrPhePheLysThrArgGluIleValLysThrAspAlaMetAsnSerLeu  
 GlnThrAlaSerPheLeuLysGluLeuLysLysIleAsnAlaArgAspTrpLeuIleAla  
 50 GlnThrMetLeuGlnGlyGlyLysArgSerSerGluValLeuSerLeuGluIleSerGln  
 IleCysPheGlnGlnAlaThrIleSerPheSerGlnLeuLysAsnArgGlnThrGluLys  
 ArgIleIleIleThrTyrProGlnLysPheMetHisPheLeuGlnGluTyrIleGlyGln

ArgArgGlyPheValPheValThrArgSerGlyLysMetValGlyLeuArgGlnIleAla  
 ArgThrPheSerGlnAlaGlyLeuGlnAlaAlaIleProPheLysIleThrProHisVal  
 5 LeuArgAlaThrAlaValThrGluTyrLysArgLeuGlyCysSerAspSerAspIleMet  
 LysValThrGlyHisAlaThrAlaLysMetIlePheAlaTyrAspLysSerSerArgGlu  
 AspAsnAlaSerLysLysMetAlaLeuIleEnd  
 10

or parts of it.

20. Recombinant expression vectors characterized by containing the genes according to claims 4-11.  
 15
21. Expression vector according to claim 20 in which the vector pertains to the pEX34 family, the cloned insert is a gene according to claims 4-11, the host cell is E.coli K12ΔH1Δtrp.
22. pO3/GO/MC1 plasmid, constituted by the recombinant expression vector pEX34 and a ORF3D insert.  
 20
23. Escherichia coli transformed with the recombinant expression vector according to claim 22 and deposited as ATCC 68315.
24. Process for preparing the immunogenic protein according to claims 12-19 in which:  
 25
  - a) an ORF is isolated according to claims 4-11
  - b) said ORF is cloned in an expression vector and the thus obtained recombinant vector is isolated
  - c) bacterial cells are transformed with the aid of a recombinant vector of stage (b)
  - d) the bacterial cells transformed as in (c) are cultivated in a suitable medium
  - e) the thus obtained protein is isolated and purified from the cell lysate.
- 30
25. Process according to claim 24 in which the vector as per stage (b) is pEX34.
26. Process according to claim 25 in which the ORF as per stage (a) is ORF3D.
- 35
27. Process according to claim 26 in which the cells as per stage (d) are the ones deposited as ATCC 68315 and the protein product is a recombinant protein (MS2-pgp3) constituted by a terminal portion generated by the vector and by the portion of the pgp3D protein.
- 40
28. Process according to claim 27 in which the cell lysate obtained from strain ATCC 68315 is partially purified by dialysis against a phosphate buffer consisting of 0.4% KCl, 0.4% KH<sub>2</sub>PO<sub>4</sub>, 16% NaCl, 2.5% NaH<sub>2</sub>PO<sub>4</sub> at 4° C for about 15 hours, the thus obtained precipitate is discarded and the protein solution is utilized both as such as an antigen in diagnostic tests and further purified.
- 45
29. Recombinant MS2-pgp3D protein resulting from the process according to claim 26 and represented by the aminoacid sequence:

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-106

MetSerLysThrThrLysLysPheAsnSerLeuCysIleAspLeuProArgAspLeuSer  
 LeuGluIleTyrGlnSerIleAlaSerValAlaThrGlySerGlyAspProHisSerAsp  
 5 AspPheThrAlaIleAlaTyrLeuArgAspGluLeuLeuThrLysHisProThrLeuGly  
 SerGlyAsnAspGluAlaThrArgArgThrLeuAlaIleAlaLysLeuArgGluAlaAsn  
 10 GlyAspArgGlyGlnIleAsnArgGluGlyPheLeuHisAspLysSerLeuSerTrpAsp  
 IleArgAlaThrGlySerMetGlyAsnSerGlyPheTyrLeuTyrAsnThrGluAsnCys  
 ValPheAlaAspAsnIleLysValGlyGlnMetThrGluProLeuLysAspGlnGlnIle  
 15 IleLeuGlyThrThrSerThrProValAlaAlaLysMetThrAlaSerAspGlyIleSer  
 LeuThrValSerAsnAsnSerSerThrAsnAlaSerIleThrIleGlyLeuAspAlaGlu  
 LysAlaTyrGlnLeuIleLeuGluLysLeuGlyAspGlnIleLeuAspGlyIleAlaAsp  
 20

ThrIleValAspSerThrValGlnAspIleLeuAspLysIleLysThrAspProSerLeu  
 25 GlyLeuLeuLysAlaPheAsnAsnPheProIleThrAsnLysIleGlnCysAsnGlyLeu  
 PheThrProSerAsnIleGluThrLeuLeuGlyGlyThrGluIleGlyLysPheThrVal  
 ThrProLysSerSerGlySerMetPheLeuValSerAlaAspIleIleAlaSerArgMet  
 30 GluGlyGlyValValLeuAlaLeuValArgGluGlyAspSerLysProCysAlaIleSer  
 TyrGlyTyrSerSerGlyIleProAsnLeuCysSerLeuArgThrSerIleThrAsnThr  
 35 GlyLeuThrProThrThrTyrSerLeuArgValGlyGlyLeuGluSerGlyValValTrp  
 ValAsnAlaLeuSerAsnGlyAsnAspIleLeuGlyIleThrAsnThrSerAsnValSer  
 PheLeuGluValIleProGlnThrAsnAlaEnd  
 40

or parts thereof.

30. Vaccine against infections caused by Chlamydia trachomatis containing an immunologically effective  
 45 amount of one of the proteins according to claims 12-19 and 29 and a pharmaceutically acceptable  
 diluent.

31. Vaccine according to claim 30 in which the protein is the one according to claim 14.

50 32. Vaccine according to claim 30 in which the protein is MS2-pgp3D2.

33. Kit for immunological RIA or ELISA assays in which the antigen utilized in the search for specific  
 antibodies to Chlamydia trachomatis is the protein according to claim 29.

55

FIG. 1A (1)

10 30 50  
 ATATTCATATTCTGTTGCCAGAAAAACACCTTTAGGCTATATTAGAGCCATCTTCTTTG  
 70 90 110  
 AAGCGTTGTCTTCTCGAGAAGATTTATCGTACGCAAATATCATCTTTGCGGTTGCGTGTC  
 130 150 170  
 CTGTGACCTTCATTATGTCGGAGTCTGAGCACCTAGGCGTTTGTACTCCGTCACAGCGG  
 190 210 230  
 TTGCTCGAAGCACGTGCGGGGTTATTTTAAAAGGGATTGCAGCTTGTAGTCCTGCTTGAG  
 250 270 290  
 AGAACGTGCGGGCGATTGTCCTTAACCCCACCATTTTCCGGAGCGAGTTACGAAGACAA  
 310 330 350  
 AACCTCTTCGTTGACCGATGTACTCTTGTAAGTGCATAAACTTCTGAGGATAAGTTA  
 370 390 410  
 TAATAATCCTCTTTTCTGTCTGACGGTTCTTAAGCTGGGAGAAAGAAATGGTAGCTTGT  
 430 450 470  
 GGAAACAAATCTGACTAATCTCCAAGCTTAAGACTTCAGAGGAGCGTTTACCTCCTTGGA  
 490 510 530  
 GCATTGTCTGGGCGATCAACCAATCCCGGGCATTGATT TTTT TAGCTCTTTTAGGAAGG  
 550 570 590  
 ATGCTGTTTGCAAACGTTCATCGCATCCGTTT TACTATTTCCCTGGTTTAAAAAATG  
 610 630 650  
 TTCGACTATTTTCTTGTTTAGAAGGTTGCGCTATAGCGACTATTCCTTGAGTCATCCTGT  
 670 690 710  
 TTAGGAATCTTGTTAAGGAAATATAGCTTGCTGCTCGAACTTGTTTAGTACCTTCGGTCC  
 730 750 770  
 AAGAAGTCTTGCGAGAGGAAACTTTTTTAATCGCATCTAGGATTAGATTATGATTTAAAA  
 790 810 830  
 GGGAAAACTCTTGCGATTTCATATCCAAGGACAATAGACCAATCTTTTCTAAAGACAAAA  
 850 870 890  
 AAGATCCTCGATATGATCTACAAGTATGTTTGTTGAGTGATGCGGTCCAATGCATAATAA  
 910 930 950  
 CTTCGAATAAGGAGAAGCTTTTCATGCGTTTCCAATAGGATTCTTGCGCAATTTTAAAA  
 970 990 1010  
 CTTCTGATAAGACTTTTCACTATATTCTAACGACATTCTTGCTGCAAAGATAAAATCC  
 1030 1050 1070  
 CTTTACCCATGAAATCCCTCGTGATATAACCTATCCGTAAAATGTCCTGATTAGTGAAT  
 1090 1110 1130  
 AATCAGGTTGTTAACAGGATAGCACGCTCGGTATTTT TATATAAACATGAAAACTCGT  
 ORF1 >> MetLysThrArg

FIG. 1A (2)

1150 1170 1190  
 TCCGAAATAGAAAATCGCATGCAAGATATCGAGTATGCGTTGTTAGGTAAAGCTCTGATA  
 SerGluIleGluAsnArgMetGlnAspIleGluTyrAlaLeuLeuGlyLysAlaLeuIle

1210 1230 1250  
 TTTGAAGACTCTACTGAGTATATTCTGAGGCAGCTTGCTAATTATGAGTTTAAAGTGTCT  
 PheGluAspSerThrGluTyrIleLeuArgGlnLeuAlaAsnTyrGluPheLysCysSer

1270 1290 1310  
 CATCATAAAAAACATATTCATAGTATTTAAACACTTAAAAGACAATGGATTACCTATAACT  
 HisHisLysAsnIlePheIleValPheLysHisLeuLysAspAsnGlyLeuProIleThr

1330 1350 1370  
 GTAGACTCGGCTTGGAAGAGCTTTTGCGGCGTCGTATCAAAGATATGGACAAATCGTAT  
 ValAspSerAlaTrpGluGluLeuLeuArgArgArgIleLysAspMetAspLysSerTyr

1390 1410 1430  
 CTCGGGTAAATGTTGCATGATGCTTTATCAAATGACAAGCTTAGATCCGTTTCTCATACG  
 LeuGlyLeuMetLeuHisAspAlaLeuSerAsnAspLysLeuArgSerValSerHisThr

1450 1470 1490  
 GTTTTCCTCGATGATTTGAGCGTGTGTAGCGCTGAAGAAAATTTGAGTAATTTTCATTTTC  
 ValPheLeuAspAspLeuSerValCysSerAlaGluGluAsnLeuSerAsnPheIlePhe

1510 1530 1550  
 CGCTCGTTTAAATGAGTACAATGAAAATCCATTGCGTAGATCTCCGTTTCTATTGCTTGAG  
 ArgSerPheAsnGluTyrAsnGluAsnProLeuArgArgSerProPheLeuLeuLeuGlu

1570 1590 1610  
 CGTATAAAGGGAAGGCTTGATAGTGCTATAGCAAAGACTTTTTCTATTTCGACGCGCTAGA  
 ArgIleLysGlyArgLeuAspSerAlaIleAlaLysThrPheSerIleArgSerAlaArg

1630 1650 1670  
 GGCCGGTCTATTTATGATATATTCTCACAGTCAGAAATTGGAGTGCTGGCTCGTATAAAA  
 GlyArgSerIleTyrAspIlePheSerGlnSerGluIleGlyValLeuAlaArgIleLys

1690 1710 1730  
 AAAAGACGAGTAGCGTTCTCTGAGAATCAAAATTCTTTCTTTGATGGCTTCCCAACAGGA  
 LysArgArgValAlaPheSerGluAsnGlnAsnSerPhePheAspGlyPheProThrGly

1750 1770 1790  
 TACAAGGATATTGATGATAAAGGAGTTATCTTAGCTAAAGGTAATTTTCGTGATTATAGCA  
 TyrLysAspIleAspAspLysGlyValIleLeuAlaLysGlyAsnPheValIleIleAla

1810 1830 1850  
 GCTAGACCATCTATAGGGAACAGCTTTAGCTATAGACATGGCGATAAATCTTGCGGTT  
 AlaArgProSerIleGlyLysThrAlaLeuAlaIleAspMetAlaIleAsnLeuAlaVal

1870 1890 1910  
 ACTCAACAGCGTAGAGTTGGTTTCCTATCTCTAGAAATGAGCGCAGGTCAAATTTGTTGAG  
 ThrGlnGlnArgArgValGlyPheLeuSerLeuGluMetSerAlaGlyGlnIleValGlu

1930 1950 1970  
 CGGATTATTGCTAATTTAACAGGAATATCTGGTGAAAAATTACAAAGAGGGGATCTCTCT  
 ArgIleIleAlaAsnLeuThrGlyIleSerGlyGluLysLeuGlnArgGlyAspLeuSer

FIG. 1A (3)

1990 2010 2030  
 AAAGAAGAATTATTCGAGTAGAAGAAGCTGGAGAAACGGTTAGAGAATCACATTTTAT  
 LysGluGluLeuPheArgValGluGluAlaGlyGluThrValArgGluSerHisPheTyr  
 2050 2070 2090  
 ATCTGCAGTGATAGTCAGTATAAGCTTAACCTTAATCGCGAATCAGATCCGGTTGCTGAGA  
 IleCysSerAspSerGlnTyrLysLeuAsnLeuIleAlaAsnGlnIleArgLeuLeuArg  
 2110 2130 2150  
 AAAGAAGATCGAGTAGACGTAATATTTATCGATTACTTGCACTGATCAACTCATCGGTT  
 LysGluAspArgValAspValIlePheIleAspTyrLeuGlnLeuIleAsnSerSerVal  
 2170 2190 2210  
 GGAGAAAATCGTCAAAATGAAATAGCAGATATATCTAGAACCTTAAGAGGTTTAGCCTCA  
 GlyGluAsnArgGlnAsnGluIleAlaAspIleSerArgThrLeuArgGlyLeuAlaSer  
 2230 2250 2270  
 GAGCTAAACATTCCATAGTTTGTGTTATCCCACTATCTAGAAAAGTTGAGGATAGAGCA  
 GluLeuAsnIleProIleValCysLeuSerGlnLeuSerArgLysValGluAspArgAla  
 2290 2310 2330  
 AATAAAGTTCCCATGCTTTCAGATTGCGAGACAGCGGTCAAATAGAGCAAGACGCAGAT  
 AsnLysValProMetLeuSerAspLeuArgAspSerGlyGlnIleGluGlnAspAlaAsp  
 2350 2370 2390  
 GTGATTTTGTGTTATCAATAGGAAGGAATCGTCTTCTAATTGTGAGATAACTGTTGGGAAA  
 ValIleLeuPheIleAsnArgLysGluSerSerSerAsnCysGluIleThrValGlyLys  
 2410 2430 2450  
 AATAGACATGGATCGGTTTTCTCTTCGGTATTACATTTTCGATCCAAAAATTAGTAAATTC  
 AsnArgHisGlySerValPheSerSerValLeuHisPheAspProLysIleSerLysPhe  
 2470 2490 2510  
 TCCGCTATTAAAAAGTATGGTAAATTATAGTAACTGCCACTTCATCAAAAAGTCCTATCC  
 SerAlaIleLysLysValTrpEnd  
 ORF2 >> MetValAsnTyrSerAsnCysHisPheIleLysSerProIleH  
 2530 2550 2570  
 ACCTTGAAAATCAGAAGTTTGAAGAAGACCTGGTCAATCTATTAAGATATCTCCCAAAT  
 isLeuGluAsnGlnLysPheGlyArgArgProGlyGlnSerIleLysIleSerProLysL  
 2590 2610 2630  
 TGGCTCAAAATGGGATGGTAGAAGTTATAGGTCTTGATTTTCTTTCATCTCATTACCATG  
 euAlaGlnAsnGlyMetValGluValIleGlyLeuAspPheLeuSerSerHisTyrHisA  
 2650 2670 2690  
 CATTAGCAGCTATCCAAAGATTACTGACCGCAACGAATTACAAGGGGAACACAAAAGGGG  
 laLeuAlaAlaIleGlnArgLeuLeuThrAlaThrAsnTyrLysGlyAsnThrLysGlyV  
 2710 2730 2750  
 TTGTTTTATCCAGAGAATCAAATAGTTTTCAATTTGAAGGATGGATACCAAGAATCCGTT  
 alValLeuSerArgGluSerAsnSerPheGlnPheGluGlyTrpIleProArgIleArgP  
 2770 2790 2810  
 TTACAAAACACTGAATTCTTAGAGGCTTATGGAGTTAAGCGGTATAAACATCCAGAAATA  
 heThrLysThrGluPheLeuGluAlaTyrGlyValLysArgTyrLysThrSerArgAsnL

FIG. 1A (4)

2830 2850 2870  
 AGTATGAGTTTAGTGGAAAAAGAAGCTGAACTGCTTTAGAACCTTATACCATTTAGGAC  
 ysTyrGluPheSerGlyLysGluAlaGluThrAlaLeuGluAlaLeuTyrHisLeuGlyH

2890 2910 2930  
 ATCAACCGTTTTTAATAGTGGCAACTAGAACTCGATGGACTAATGGAACACAAATAGTAG  
 isGlnProPheLeuIleValAlaThrArgThrArgTrpThrAsnGlyThrGlnIleValA

2950 2970 2990  
 ACCGTTACCAAACCTCTTCTCCGATCATTAGGATTTACGAAGGATGGGAAGGTTTAACTG  
 spArgTyrGlnThrLeuSerProIleIleArgIleTyrGluGlyTrpGluGlyLeuThra

3010 3030 3050  
 ACGAAGAAAATATAGATATAGACTTAACACCTTTTAATTCACCACCTACACGGAAACATA  
 spGluGluAsnIleAspIleAspLeuThrProPheAsnSerProProThrArgLysHisL

3070 3090 3110  
 AAGGGTTCGTTGTAGAGCCATGTCCTATCTTGGTAGATCAAATAGAAATCCTACTTTGTAA  
 ysGlyPheValValGluProCysProIleLeuValAspGlnIleGluSerTyrPheValI

3130 3150 3170  
 TCAAGCCTGCAAAATGTATACCAAGAAATAAAAAATGCGTTTCCCAAATGCATCAAAGTATG  
 leLysProAlaAsnValTyrGlnGluIleLysMetArgPheProAsnAlaSerLysTyrA

3190 3210 3230  
 CTTACACATTTATCGACTGGGTGATTACAGCAGCTGCGAAAAAGAGACGAAATTAAC TA  
 laTyrThrPheIleAspTrpValIleThrAlaAlaAlaLysLysArgArgLysLeuThrL

3250 3270 3290  
 AGGATAATTCTTGGCCAGAAAACCTGTATTAAACGTTAACGTTAAAGTCTTGCATATA  
 ysAspAsnSerTrpProGluAsnLeuLeuLeuAsnValAsnValLysSerLeuAlaTyrI

3310 3330 3350  
 TTTTAAGGATGAATCGGTACATCTGTACAAGGAACTGGAAAAAAATCGAGTTAGCTATCG  
 leLeuArgMetAsnArgTyrIleCysThrArgAsnTrpLysLysIleGluLeuAlaIleA

3370 3390 3410  
 ATAAATGTATAGAAATCGCCATTTCAGCTTGGCTGGTTATCTAGAAGAAAACGCATTGAAT  
 spLysCysIleGluIleAlaIleGlnLeuGlyTrpLeuSerArgArgLysArgIleGluP

3430 3450 3470  
 TTCTGGATTCTTCTAAACTCTCTAAAAAGAAATTCTATATCTAAATAAAGAGCGCTTTG  
 heLeuAspSerSerLysLeuSerLysLysGluIleLeuTyrLeuAsnLysGluArgPheG

3490 3510 3530  
 AAGAAATAACTAAGAAATCTAAAGAACAAATGGAACAATTAGAACAAGAATCTATTAATT  
 luGluIleThrLysLysSerLysGluGlnMetGluGlnLeuGluGlnGluSerIleAsnE

3550 3570 3590  
 AATAGCAAGCTTGAAACTAAAAACCTAATTTATTTAAAGCTCAAAATAAAAAAGAGTTTT  
 nd

3610 3630 3650  
 AAAATGGGAAATTCTGGTTTTTTATTTGTATAACACTGAAAACCTGCGTCTTTGCTGATAAT  
 ORF3>> MetGlyAsnSerGlyPheTyrLeuTyrAsnThrGluAsnCysValPheAlaAspAsn

3670 3690 3710  
 ATCAAAGTTGGGCAAATGACAGAGCCGCTCAAGGACCAGCAAATAATCCTTGGGACAACA  
 IleLysValGlyGlnMetThrGluProLeuLysAspGlnGlnIleIleLeuGlyThrThr

FIG. 14 (5)

3730 3750 3770  
 TCAACACCTGTCGCAGCCAAAATGACAGCTTCTGATGGAATATCTTTAACAGTCTCCAAT  
 SerThrProValAlaAlaLysMetThrAlaSerAspGlyIleSerLeuThrValSerAsn  
 3790 3810 3830  
 AATTCATCAACCAATGCTTCTATTACAATTGGTTTGGATGCGGAAAAAGCTTACCAGCTT  
 AsnSerSerThrAsnAlaSerIleThrIleGlyLeuAspAlaGluLysAlaTyrGlnLeu  
 3850 3870 3890  
 ATTCTAGAAAAGTTGGGAGATCAAATTCTTGATGGAATTGCTGATACTATTGTTGATAGT  
 IleLeuGluLysLeuGlyAspGlnIleLeuAspGlyIleAlaAspThrIleValAspSer  
 3910 3930 3950  
 ACAGTCCAAGATATTTTAGACAAAATCAAACAGACCCTTCTCTAGGTTTGTGAAAGCT  
 ThrValGlnAspIleLeuAspLysIleLysThrAspProSerLeuGlyLeuLeuLysAla  
 3970 3990 4010  
 TTTAACAACCTTTCCAATCACTAATAAAATTCAATGCAACGGGTATTCACTCCCAGTAAC  
 PheAsnAsnPheProIleThrAsnLysIleGlnCysAsnGlyLeuPheThrProSerAsn  
 4030 4050 4070  
 ATTGAACTTTATTAGGAGGAACTGAAATAGGAAAATTCACAGTCACACCCAAAAGCTCT  
 IleGluThrLeuLeuGlyGlyThrGluIleGlyLysPheThrValThrProLysSerSer  
 4090 4110 4130  
 GGGAGCATGTTCTTAGTCTCAGCAGATATTATTGCATCAAGAATGGAAGGCGGCGTTGTT  
 GlySerMetPheLeuValSerAlaAspIleIleAlaSerArgMetGluGlyGlyValVal  
 4150 4170 4190  
 CTAGCTTTGGTACGAGAAGGTGATTCTAAGCCCTGCGCGATTAGTTATGGATACTCATCA  
 LeuAlaLeuValArgGluGlyAspSerLysProCysAlaIleSerTyrGlyTyrSerSer  
 4210 4230 4250  
 GGCATTCTTAATTTATGTAGTCTAAGAACCAGTATTACTAATACAGGATTGACTCCGACA  
 GlyIleProAsnLeuCysSerLeuArgThrSerIleThrAsnThrGlyLeuThrProThr  
 4270 4290 4310  
 ACGTATTCAATTACGTGTAGGCGGTTTAGAAAAGCGGTGTGGTATGGGTTAATGCCCTTTCT  
 ThrTyrSerLeuArgValGlyGlyLeuGluSerGlyValValTrpValAsnAlaLeuSer  
 4330 4350 4370  
 AATGGCAATGATATTTTAGGAATAACAAATACTTCTAATGTATCTTTTTAGAGGTAATA  
 AsnGlyAsnAspIleLeuGlyIleThrAsnThrSerAsnValSerPheLeuGluValIle  
 4390 4410 4430  
 CCTCAAACAAACGCTTAAACAATTTTTATTGGATTTTTCTTATAGGTTTTATATTTAGAG  
 ProGlnThrAsnAlaEnd  
 4450 4470 4490  
 AAAACAGTTCGAATTACGGGGTTTGTATGCAAAATAAAAGAAAAGTGAGGGACGATTTT  
 ORF4 >> MetGlnAsnLysArgLysValArgAspAspPhe  
 4510 4530 4550  
 ATTAATAATGTTAAAGATGTGAAAAAGATTTCCTCCGAATTAGACCTAAAAATACGAGTA  
 IleLysIleValLysAspValLysLysAspPheProGluLeuAspLeuLysIleArgVal  
 4570 4590 4610  
 AACAAGGAAAAAGTAACTTTCTTAAATTCCTCCCTTAGAACTCTACCATAAAAGTGTCTCA  
 AsnLysGluLysValThrPheLeuAsnSerProLeuGluLeuTyrHisLysSerValSer

FIG. 1A (6)

4630 4650 4670  
 CTAATTCTAGGACTGCTTCAACAAATAGAAAACCTCTTTAGGATTATTCCCAGACTCTCCT  
 LeuIleLeuGlyLeuLeuGlnGlnIleGluAsnSerLeuGlyLeuPheProAspSerPro  
 4690 4710 4730  
 GTTCTTGAAAAATTAGAGGATAACAGTTTAAAGCTAAAAAAGGCTTTGATTATGCTTATC  
 ValLeuGluLysLeuGluAspAsnSerLeuLysLeuLysLysAlaLeuIleMetLeuIle  
 4750 4770 4790  
 TTGTCTAGAAAAGACATGTTTTCCAAGGCTGAATAGACAACTTACTCTAACGTTGGAGTT  
 LeuSerArgLysAspMetPheSerLysAlaGluEnd  
 4810 4830 4850  
 GATTTGCACACCTTAGTTTTTGTCTCTTTTAAGGGAGGAAGTGGAAAAACAACACTTTCT  
 ORF5 >> LeuHisThrLeuValPheCysSerPheLysGlyGlyThrGlyLysThrThrLeuSer  
 4870 4890 4910  
 CTAACGTGGGATGCAACTTGGCCCAATTTTTAGGGAAAAAAGTGTTACTTGCTGACCTA  
 LeuAsnValGlyCysAsnLeuAlaGlnPheLeuGlyLysLysValLeuLeuAlaAspLeu  
 4930 4950 4970  
 GACCCGCAATCCAATTTATCTTCTGGATTGGGGCTAGTGTCAGAAAGTGACCAAAAAGGC  
 AspProGlnSerAsnLeuSerSerGlyLeuGlyAlaSerValArgSerAspGlnLysGly  
 4990 5010 5030  
 TTGCACGACATAGTATACACATCAAACGATTTAAATCAATCATTGCGAAACAAAAA  
 LeuHisAspIleValTyrThrSerAsnAspLeuLysSerIleIleCysGluThrLysLys  
 5050 5070 5090  
 GATAGTGTGGACCTAATTCCTGCATCATTTCATCCGAACAGTTTAGAGAATTGGATATT  
 AspSerValAspLeuIleProAlaSerPheSerSerGluGlnPheArgGluLeuAspIle  
 5110 5130 5150  
 CATAGAGGACCTAGTAACAACTTAAAGTTATTTCTGAATGAGTACTGCGCTCCTTTTTAT  
 HisArgGlyProSerAsnAsnLeuLysLeuPheLeuAsnGluTyrCysAlaProPheTyr  
 5170 5190 5210  
 GACATCTGCATAATAGACACTCCACCTAGCCTAGGAGGGTTAACGAAAGAAGCTTTTGTT  
 AspIleCysIleIleAspThrProProSerLeuGlyGlyLeuThrLysGluAlaPheVal  
 5230 5250 5270  
 GCAGGAGACAAATTAATTGCTTGTTTAACTCCAGAACCTTTTTCTATTCTAGGGTTACAA  
 AlaGlyAspLysLeuIleAlaCysLeuThrProGluProPheSerIleLeuGlyLeuGln  
 5290 5310 5330  
 AAGATACGTGAATTCTTAAGTTCGGTCGGAACCTGAAGAAGAACACATTCTTGAATA  
 LysIleArgGluPheLeuSerSerValGlyLysProGluGluGluHisIleLeuGlyIle  
 5350 5370 5390  
 GCTTTGTCTTTTTGGGATGATCGTAACCTCGACTAACCAAATGTATATAGACATTATCGAG  
 AlaLeuSerPheTrpAspAspArgAsnSerThrAsnGlnMetTyrIleAspIleIleGlu  
 5410 5430 5450  
 TCTATTTACAAAAACAAGCTTTTTTCAACAAAAATTCGTCGAGATATTTCTCTCAGCCGT  
 SerIleTyrLysAsnLysLeuPheSerThrLysIleArgArgAspIleSerLeuSerArg  
 5470 5490 5510  
 TCTCTTCTTAAAGAAGATTCTGTAGCTAATGTCTATCCAAATTCTAGGGCCGAGAAGAT  
 SerLeuLeuLysGluAspSerValAlaAsnValTyrProAsnSerArgAlaAlaGluAsp

FIG. 1A (7)

5530 5550 5570  
 ATTCTGAAGTTAACGCATGAAATAGCAAATATTTTGCATATCGAATATGAACGAGATTAC  
 IleLeuLysLeuThrHisGluIleAlaAsnIleLeuHisIleGluTyrGluArgAspTyr  
 5590 5610 5630  
 TCTCAGAGGACAACGTGAACAACTAAAAAAGAAGCGGATGTCTTTTTTAAAAAAATC  
 SerGlnArgThrThrEnd  
 ORF6 >> ValAsnLysLeuLysLysGluAlaAspValPhePheLysLysAsnG  
 5650 5670 5690  
 AAACGCGCTTCTCTAGATTTTAAGAAGACGCTTCCCTCCATTGAACTATTCTCAGCAA  
 lnThrAlaAlaSerLeuAspPheLysLysThrLeuProSerIleGluLeuPheSerAlaT  
 5710 5730 5750  
 CTTTGAATTCTGAGGAAAGTCAGAGTTTGGATCGATTATTTTTATCAGAGTCCCAAACT  
 hrLeuAsnSerGluGluSerGlnSerLeuAspArgLeuPheLeuSerGluSerGlnAsnT  
 5770 5790 5810  
 ATTCGGATGAAGAATTTTATCAAGAAGACATCCTAGCGGTAAAACTGCTTACTGGTCAGA  
 yrSerAspGluGluPheTyrGlnGluAspIleLeuAlaValLysLeuLeuThrGlyGlnI  
 5830 5850 5870  
 TAAATCCATACAGAAGCAACACGTACTTCTTTTAGGAGAAAAATCTATAATGCTAGAA  
 leLysSerIleGlnLysGlnHisValLeuLeuLeuGlyGluLysIleTyrAsnAlaArgL  
 5890 5910 5930  
 AAATCCTGAGTAAGGATCACTTCTCCTCAACAACTTTTTTCATCTTGATAGAGTTAGTTT  
 ysIleLeuSerLysAspHisPheSerSerThrThrPheSerSerTrpIleGluLeuValP  
 5950 5970 5990  
 TTAGAATAAGTCTTCTGCTTACAATGCTCTTGCATATTACGAGCTTTTTATAAACCTCC  
 heArgThrLysSerSerAlaTyrAsnAlaLeuAlaTyrTyrGluLeuPheIleAsnLeuP  
 6010 6030 6050  
 CCAACCAAACCTCTACAAAAAGAGTTTCAATCGATCCCCTATAAATCCGCATATATTTTGG  
 roAsnGlnThrLeuGlnLysGluPheGlnSerIleProTyrLysSerAlaTyrIleLeuA  
 6070 6090 6110  
 CCGCTAGAAAAGGCGATTAAAAACCAAGGTCGATGTGATAGGGAAGTATGTGGAATGT  
 laAlaArgLysGlyAspLeuLysThrLysValAspValIleGlyLysValCysGlyMetS  
 6130 6150 6170  
 CGAACTCATCGGCGATAAGGGTGTTGGATCAATTTCTTCTTCATCTAGAAACAAAGACG  
 erAsnSerSerAlaIleArgValLeuAspGlnPheLeuProSerSerArgAsnLysAspV  
 6190 6210 6230  
 TTAGAGAAACGATAGATAAGTCTGATTGAGAGAAGAATCGCCAATTATCTGATTTCTTAA  
 alArgGluThrIleAspLysSerAspSerGluLysAsnArgGlnLeuSerAspPheLeuI  
 6250 6270 6290  
 TAGAGATACTTCGCATCATGTGTTCCGGAGTTTCTTTGTCCTCCTATAACGAAAATCTTC  
 leGluIleLeuArgIleMetCysSerGlyValSerLeuSerSerTyrAsnGluAsnLeuL  
 6310 6330 6350  
 TACAACAGCTTTTTGAACTTTTAAGCAAAAGAGCTGATCCTCTGTCAGCTCATATATAT  
 euGlnGlnLeuPheGluLeuPheLysGlnLysSerEnd

FIG. 1A (8)

6370 6390 6410  
 ATATCTATTATATATATATATATTTAGGGATTTGATTTTCACGAGAGAGATTTGCAACTCTTG  
 6430 6450 6470  
 GTGGTAGACTTTGCAACTCTTGGTGGTAGACTTTGCAACTCTTGGTGGTAGACTTTGCAA  
 6490 6510 6530  
 CTCTTGGTGGTAGACTTGGTCATAATGGACTTTTGTTAAAAATTTATTAAAACTTAGA  
 6550 6570 6590  
 GCTCCGATTTTGAATAGCTTTGGTTAAGAAAATGGGCTCGATGGCTTTCCATAAAAGTAG  
 ORF7 >> LeuValLysLysMetGlySerMetAlaPheHisLysSerAr  
 6610 6630 6650  
 ATTGTTTTTAACCTTTTGGGGACGCGTCGGAAATTTGGTTATCTACTTTATCTTATCTAAC  
 gLeuPheLeuThrPheGlyAspAlaSerGluIleTrpLeuSerThrLeuSerTyrLeuTh  
 6670 6690 6710  
 TAGAAAAAATTATGCGTCTGGGATTAACCTTTCTGTTTCTTTAGAGATTCTGGATTTATC  
 rArgLysAsnTyrAlaSerGlyIleAsnPheLeuValSerLeuGluIleLeuAspLeuSe  
 6730 6750 6770  
 GGAAACCTTGATAAAGGCTATTTCTCTTGACCACAGCGAATCTTTGTTTAAATCAAGTC  
 rGluThrLeuIleLysAlaIleSerLeuAspHisSerGluSerLeuPheLysIleLysSe  
 6790 6810 6830  
 TCTAGATGTTTTTAATGGAAAAGTTGTTTCAGAGGCATCTAAACAGGCTAGAGCGGCATG  
 rLeuAspValPheAsnGlyLysValValSerGluAlaSerLysGlnAlaArgAlaAlaCy  
 6850 6870 6890  
 CTACATATCTTTTACAAAGTTTTTGTATAGATTGACCAAGGGATATATTAAACCCGCTAT  
 sTyrIleSerPheThrLysPheLeuTyrArgLeuThrLysGlyTyrIleLysProAlaIl  
 6910 6930 6950  
 TCCATTGAAAGATTTTGGAAACACTACATTTTTTAAATCCGAGACAAAATCAAAACAGA  
 eProLeuLysAspPheGlyAsnThrThrPhePheLysIleArgAspLysIleLysThrGl  
 6970 6990 7010  
 ATCGATTTCTAAGCAGGAATGGACAGTTTTTTTTGAAGCGCTCCGGATAGTGAATTATAG  
 uSerIleSerLysGlnGluTrpThrValPhePheGluAlaLeuArgIleValAsnTyrAr  
 7030 7050 7070  
 AGACTATTTAATCGGTAAATTGATTGTACAAGGGATCCGTAAGTTAGACGAAATTTTGTC  
 gAspTyrLeuIleGlyLysLeuIleValGlnGlyIleArgLysLeuAspGluIleLeuSe  
 7090 7110 7130  
 TTTGCGCACAGACGATCTATTTTTTGCATCCAATCAGATTTCTTTTCGCATTAAAAAAG  
 rLeuArgThrAspAspLeuPhePheAlaSerAsnGlnIleSerPheArgIleLysLysAr  
 7150 7170 7190  
 ACAGAATAAAGAAACCAAAATTCTAATCACATTTCTATCAGCTTAATGGAAGAGTTGCA  
 gGlnAsnLysGluThrLysIleLeuIleThrPheProIleSerLeuMetGluGluLeuGl  
 7210 7230 7250  
 AAAATACACTTGTGGGAGAAATGGGAGAGTATTTGTTTCTAAAATAGGGATTCCTGTAAC  
 nLysTyrThrCysGlyArgAsnGlyArgValPheValSerLysIleGlyIleProValth

FIG. 1A (9)

7270	7290	7310
AACAAGTCAGGTTGCGCATAATTTTAGGCTTGACAGAGTTCATAGTGCTATGAAAATAAA		
rThrSerGlnValAlaHisAsnPheArgLeuAlaGluPheHisSerAlaMetLysIleLy		
7330	7350	7370
AATTACTCCCAGAGTACTTCGTGCAAGCGCTTTGATTCATTTAAAGCAAATAGGATTAAA		
sIleThrProArgValLeuArgAlaSerAlaLeuIleHisLeuLysGlnIleGlyLeuLy		
7390	7410	7430
AGATGAGGAAATCATGCGTATTTCTGTCTTTTCATCGAGACAAAGTGTGTGTTCTTATTG		
sAspGluGluIleMetArgIleSerCysLeuSerSerArgGlnSerValCysSerTyrCy		
7450	7470	7490
TTCTGGGGAAGAGGTAATTCCTCTAGTACAAACACCCACAATATTGTGATATAATTAAAA		
sSerGlyGluGluValIleProLeuValGlnThrProThrIleLeuEnd		

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FIG. 1B (1)

GCATGCGATTTTCTATTTTCGGAACGAGTTTTCATGTTTATATAAAAAAATACCGAGCGTG  
 CTATCCTGTAAACAACCTGATTATTTCACTAATCAGGACATTTTACGGATAGGTTATATC  
 ACGAGGGATTTTCATGGGTAAAGGGATTTTATCTTTGCAGCAAGAAATGTCGTTAGAATAT  
 ORF8 >> MetGlyLysGlyIleLeuSerLeuGlnGlnGluMetSerLeuGluTyr  
 AGTGAAAAGTCTTATCAGGAAGTTTTAAAAATTCGCCAAGAATCCTATTGGAAACGCATG  
 SerGluLysSerTyrGlnGluValLeuLysIleArgGlnGluSerTyrTrpLysArgMet  
 AAAAGCTTCTCCTTATTCGAAGTTATTATGCATTGGACCGCATCACTCAACAAACATACT  
 LysSerPheSerLeuPheGluValIleMetHisTrpThrAlaSerLeuAsnLysHisThr  
 TG TAGATCATATCGAGGATCTTTTTGTCTTTAGAAAAGATTGGTCTATTGTCCTTGGAT  
 CysArgSerTyrArgGlySerPheLeuSerLeuGluLysIleGlyLeuLeuSerLeuAsp  
 ATGAATCTGCAAGAGTTTTCCCTTTTAAATCATAATCTAATCCTAGATGCGATTAAAAAA  
 MetAsnLeuGlnGluPheSerLeuLeuAsnHisAsnLeuIleLeuAspAlaIleLysLys  
 GTTTCCTCTGCCAAGACTTCTTGGACCGAAGGTACTAAACAAGTTCGAGCAGCAAGCTAT  
 ValSerSerAlaLysThrSerTrpThrGluGlyThrLysGlnValArgAlaAlaSerTyr  
 ATTCCTTAACAAGATTCCTAAACAGGATGACTCAAGGAATAGTCGCTATAGCGCAACCT  
 IleSerLeuThrArgPheLeuAsnArgMetThrGlnGlyIleValAlaIleAlaGlnPro  
 TCTAAACAAGAAAATAGTCGAACATTTTTTAAACCAGGGAAATAGTAAAAACGGATGCG  
 SerLysGlnGluAsnSerArgThrPhePheLysThrArgGluIleValLysThrAspAla  
 ATGAACAGTTTGCAAACAGCATCCTTCCTAAAAGAGCTAAAAAAAATCAATGCCCGGGAT  
 MetAsnSerLeuGlnThrAlaSerPheLeuLysGluLeuLysLysIleAsnAlaArgAsp  
 TGGTTGATCGCCCAGACAATGCTCCAAGGAGGTAAACGCTCCTCTGAAGTCTTAAGCTTG  
 TrpLeuIleAlaGlnThrMetLeuGlnGlyGlyLysArgSerSerGluValLeuSerLeu  
 GAGATTAGTCAGATTTGTTTCCAACAAGCTACCATTCTTTCTCCAGCTTAAGAACCGT  
 GluIleSerGlnIleCysPheGlnGlnAlaThrIleSerPheSerGlnLeuLysAsnArg  
 CAGACAGAAAAGAGGATTATTATACTTATCCTCAGAAGTTTATGCACTTTCTACAAGAG  
 GlnThrGluLysArgIleIleIleThrTyrProGlnLysPheMetHisPheLeuGlnGlu

FIG. 1B (2)

TACATCGGTCAACGAAGAGGTTTTGTCTTCGTAACGCTCCGGAAAAATGGTGGGGTTA  
TyrIleGlyGlnArgArgGlyPheValPheValThrArgSerGlyLysMetValGlyLeu

AGGCAAATCGCCCGCACGTTCTCTCAAGCAGGACTACAAGCTGCAATCCCTTTTAAATA  
ArgGlnIleAlaArgThrPheSerGlnAlaGlyLeuGlnAlaAlaIleProPheLysIle

ACCCCGCACGTGCTTCGAGCAACCGCTGTGACGGAGTACAAACGCCTAGGGTGCTCAGAC  
ThrProHisValLeuArgAlaThrAlaValThrGluTyrLysArgLeuGlyCysSerAsp

TCCGACATAATGAAGGTCACAGGACACGCAACCGCAAAGATGATATTTGCGTACGATAAA  
SerAspIleMetLysValThrGlyHisAlaThrAlaLysMetIlePheAlaTyrAspLys

TCTTCTCGAGAAGACAACGCTTCAAAGAAGATGGCTCTAATATAGCCTAAAGGTGTTTTT  
SerSerArgGluAspAsnAlaSerLysLysMetAlaLeuIleEnd

TCTGGCAACAGAATATGAATAT

FIG. 2

3610 3630 3650  
 AAAATGGGAAATTCTGGTTTTTATTTGTATAACACTGAAACTGCGTCTTTGCTGATAAT  
 ORF3>> MetGlyAsnSerGlyPheTyrLeuTyrAsnThrGluAsnCysValPheAlaAspAsn  
  
 3670 3690 3710  
 ATCAAAGTTGGGCAAATGACAGAGCCGCTCAAGGACCAGCAAATAATCCTTGGGACAACA  
 IleLysValGlyGlnMetThrGluProLeuLysAspGlnGlnIleIleLeuGlyThrThr  
  
 3730 3750 3770  
 TCAACACCTGTGCGAGCCAAAATGACAGCTTCTGATGGAATATCTTTAACAGTCTCCAAT  
 SerThrProValAlaAlaLysMetThrAlaSerAspGlyIleSerLeuThrValSerAsn  
  
 3790 3810 3830  
 AATTCATCAACCAATGCTTCTATTACAATTGGTTTGGATGCGGAAAAAGCTTACCAGCTT  
 AsnSerSerThrAsnAlaSerIleThrIleGlyLeuAspAlaGluLysAlaTyrGlnLeu  
  
 3850 3870 3890  
 ATTCTAGAAAAGTTGGGAGATCAAATTCTTGATGGAATTGCTGATACTATTGTTGATAGT  
 IleLeuGluLysLeuGlyAspGlnIleLeuAspGlyIleAlaAspThrIleValAspSer  
  
 3910 3930 3950  
 ACAGTCCAAGATATTTTAGACAAAATCAAACAGACCCTTCTCTAGGTTTGTGAAAGCT  
 ThrValGlnAspIleLeuAspLysIleLysThrAspProSerLeuGlyLeuLeuLysAla  
  
 3970 3990 4010  
 TTTAACAACCTTTCCAATCACTAATAAAATTCAATGCAACGGGTATTCACTCCCAGTAAC  
 PheAsnAsnPheProIleThrAsnLysIleGlnCysAsnGlyLeuPheThrProSerAsn  
  
 4030 4050 4070  
 ATTGAACTTTATTAGGAGGAACTGAAATAGGAAAATTCACAGTCACACCCAAAAGCTCT  
 IleGluThrLeuLeuGlyGlyThrGluIleGlyLysPheThrValThrProLysSerSer  
  
 4090 4110 4130  
 GGGAGCATGTTCTTAGTCTCAGCAGATATTATTGCATCAAGAATGGAAGGCGGCGTTGTT  
 GlySerMetPheLeuValSerAlaAspIleIleAlaSerArgMetGluGlyGlyValVal  
  
 4150 4170 4190  
 CTAGCTTTGGTACGAGAAGGTGATTCTAAGCCCTGCGCGATTAGTTATGGATACTCATCA  
 LeuAlaLeuValArgGluGlyAspSerLysProCysAlaIleSerTyrGlyTyrSerSer  
  
 4210 4230 4250  
 GGCATTCTAATTTATGTAGTCTAAGAACCAGTATTACTAATACAGGATTGACTCCGACA  
 GlyIleProAsnLeuCysSerLeuArgThrSerIleThrAsnThrGlyLeuThrProThr  
  
 4270 4290 4310  
 ACGTATTCATTACGTGTAGGCGGTTTAGAAAGCGGTGTGGTATGGGTTAATGCCCTTTCT  
 ThrTyrSerLeuArgValGlyGlyLeuGluSerGlyValValTrpValAsnAlaLeuSer  
  
 4330 4350 4370  
 AATGGCAATGATATTTTAGGAATAACAAATACTTCTAATGTATCTTTTTTAGAGGTAATA  
 AsnGlyAsnAspIleLeuGlyIleThrAsnThrSerAsnValSerPheLeuGluValIle  
  
 4390 4410 4430  
 CCTCAAACAAACGCTTAAACAATTTTATTGGATTTTCTTATAGGTTTTATATTTAGAG  
 ProGlnThrAsnAlaEnd

FIG. 3

-106

MetSerLysThrThrLysLysPheAsnSerLeuCysIleAspLeuProArgAspLeuSer  
 LeuGluIleTyrGlnSerIleAlaSerValAlaThrGlySerGlyAspProHisSerAsp  
 AspPheThrAlaIleAlaTyrLeuArgAspGluLeuLeuThrLysHisProThrLeuGly  
 SerGlyAsnAspGluAlaThrArgArgThrLeuAlaIleAlaLysLeuArgGluAlaAsn  
 GlyAspArgGlyGlnIleAsnArgGluGlyPheLeuHisAspLysSerLeuSerTrpAsp  
 IleArgAlaThrGlySerMetGlyAsnSerGlyPheTyrLeuTyrAsnThrGluAsnCys  
 ValPheAlaAspAsnIleLysValGlyGlnMetThrGluProLeuLysAspGlnGlnIle  
 IleLeuGlyThrThrSerThrProValAlaAlaLysMetThrAlaSerAspGlyIleSer  
 LeuThrValSerAsnAsnSerSerThrAsnAlaSerIleThrIleGlyLeuAspAlaGlu  
 LysAlaTyrGlnLeuIleLeuGluLysLeuGlyAspGlnIleLeuAspGlyIleAlaAsp  
 ThrIleValAspSerThrValGlnAspIleLeuAspLysIleLysThrAspProSerLeu  
 GlyLeuLeuLysAlaPheAsnAsnPheProIleThrAsnLysIleGlnCysAsnGlyLeu  
 PheThrProSerAsnIleGluThrLeuLeuGlyGlyThrGluIleGlyLysPheThrVal  
 ThrProLysSerSerGlySerMetPheLeuValSerAlaAspIleIleAlaSerArgMet  
 GluGlyGlyValValLeuAlaLeuValArgGluGlyAspSerLysProCysAlaIleSer  
 TyrGlyTyrSerSerGlyIleProAsnLeuCysSerLeuArgThrSerIleThrAsnThr  
 GlyLeuThrProThrThrTyrSerLeuArgValGlyGlyLeuGluSerGlyValValTrp  
 ValAsnAlaLeuSerAsnGlyAsnAspIleLeuGlyIleThrAsnThrSerAsnValSer  
 PheLeuGluValIleProGlnThrAsnAlaEnd



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Application Number

EP 91 10 6110

PAGE1

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Place of search BERLIN		Date of completion of the search 19 MAY 1992	Examiner JULIA P.
<b>CATEGORY OF CITED DOCUMENTS</b> X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons A : member of the same patent family, corresponding document			



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## EUROPEAN SEARCH REPORT

Application Number

EP 91 10 6110  
PAGE2

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